

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 03:05:25 ; Search time 1130 Seconds
(without alignments)
8759.686 Million cell updates/sec

Title: US-10-771-417-6

Perfect score: 1197

Sequence: 1 atgcacacgtggctacgtc.....aggacaagccctctctga 1197

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1197	100.0	1197	5	US-10-225-567A-476
2	1197	100.0	1197	6	US-10-295-027-747
3	1197	100.0	1197	6	US-10-295-027-822
4	1197	100.0	1197	8	US-10-771-417-6
5	1197	100.0	1197	9	US-10-847-918-9
6	1197	100.0	1450	8	US-10-833-829-1
7	1195.4	99.9	1197	3	US-09-796-338A-18
8	1195.4	99.9	1197	3	US-09-897-201-1
9	1195.4	99.9	1197	5	US-10-188-425-1
10	1195.4	99.9	1197	5	US-10-282-837-18
11	1195.4	99.9	1197	6	US-10-145-586-18
12	1195.4	99.9	1197	6	US-10-407-079-94
13	1195.4	99.9	1609	3	US-09-796-338A-16
14	1195.4	98.9	1609	5	US-10-282-837-16
15	1195.4	99.9	1609	6	US-10-145-586-16
16	1195.4	99.9	1609	6	US-10-407-079-92
17	1195.4	99.9	1609	8	US-10-757-262-31
18	1195.4	99.9	1617	6	US-10-241-220-48
19	1195.4	99.9	1617	8	US-10-872-972-48
20	1195.4	99.9	1617	8	US-10-872-991-48
21	1194.6	99.8	1197	9	US-10-451-002-1
22	1194.6	99.8	1197	9	US-10-451-002-3
23	1193.8	99.7	1197	8	US-10-782-021-1

ALIGNMENTS

RESULT 1

US-10-225-567A-476

; Sequence 476, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: Lifespan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 476

; LENGTH: 1197

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-476

Query Match	100.0%	Score 1197;	DB 5;	Length 1197;
Best Local Similarity	100.0%	Pred. No. 3e-246;		
Matches 1197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCACACCGTGGCTACGTCGGGACCCCAACCGCTCTGGGGGGCACCGGCGCAACGCTCC 60		
Db	1	ATGCACACCGTGGCTACGTCGGGACCCCAACCGCTCTGGGGGGCACCGGCGCAACGCTCC 60		
QY	61	GGCTGCCCGGGCTGTGGGGCCCAACGCTTCGACCGGCCAGTCCCTTCGCGGGGGCGGTG 120		
Db	61	GGCTGCCCGGGCTGTGGGGCCCAACGCTTCGACCGGCCAGTCCCTTCGCGGGGGCGGTG 120		
QY	121	GACGCTGGCTCGTGGCGGCTCTTCTTCGCGGGCTGTGCTGGGCTGTGGGGGAAC 180		
Db	121	GACGCTGGCTCGTGGCGGCTCTTCTTCGCGGGCTGTGCTGGGCTGTGGGGGAAC 180		
QY	181	TCGCTGGTCACTACGTCACTTCGCGGCCCAAGCCGATGCGGACCGTGCACCACTTCTAC 240		
Db	181	TCGCTGGTCACTACGTCACTTCGCGGCCCAAGCCGATGCGGACCGTGCACCACTTCTAC 240		
QY	241	ATCGCCAACTGGGGGCCACGAGTGAACCTTCCTCTGTGCTGGTCCCTTACAGGCC 300		
Db	241	ATCGCCAACTGGGGGCCACGAGTGAACCTTCCTCTGTGCTGGTCCCTTACAGGCC 300		

Qy	301	CTGCTGTACCGCTGCCCGGCTGGTGTCTGGCGACTTCATGTGCAAGTTGGTCAACTAC	360
Db	301	CTGCTGTACCGCTGCCCGGCTGGTGTCTGGCGACTTCATGTGCAAGTTGGTCAACTAC	360
Qy	361	ATCCAGCAGGTTCTCGGTGCAGGCCACGTGTGCCACTCTGACCGGCATGAGTGTGGACCGC	420
Db	361	ATCCAGCAGGTTCTCGGTGCAGGCCACGTGTGCCACTCTGACCGGCATGAGTGTGGACCGC	420
Qy	421	TGGTACGTGACGCGTTCCCGTTGCGGCCCTGACCGCGCAGCGCCCGCTGCGCGCTG	480
Db	421	TGGTACGTGACGCGTTCCCGTTGCGGCCCTGACCGCGCAGCGCCCGCTGCGCGCTG	480
Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCCCTG	540
Db	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCCCTG	540
Qy	541	CACCGCCTGTCAACCGGCGCGCGCTTACTGTGAGTGAGGCGCTTCCCGACGCGCGCCCTG	600
Db	541	CACCGCCTGTCAACCGGCGCGCGCTTACTGTGAGTGAGGCGCTTCCCGACGCGCGCCCTG	600
Qy	601	GAGCGCGCTTTCGACCTGTGTAACACTGTGTGCGCTGTACTGTGCTGCGCTGTCTGCCAC	660
Db	601	GAGCGCGCTTTCGACCTGTGTAACACTGTGTGCGCTGTACTGTGCTGCGCTGTCTGCCAC	660
Qy	661	TGCGCCTGTCTATGCGGCCATGCTCGGCCACTGTGGCCCGGCTGCGCGCTGCGCCCGCGGCC	720
Db	661	TGCGCCTGTCTATGCGGCCATGCTCGGCCACTGTGGCCCGGCTGCGCGCTGCGCCCGCGGCC	720
Qy	721	GCCGATAGCGCCTTCGAGGGGCAAGTGTGTGGCAGAGCGCGCAGCGCGCTGCGGGCCAA	780
Db	721	GCCGATAGCGCCTTCGAGGGGCAAGTGTGTGGCAGAGCGCGCAGCGCGCTGCGGGCCAA	780
Qy	781	GTCTCGCGGCTGTGTGGCGCGTGGTCTGTCTTTCGCGCGCTGTCTGGGCCCCCATCCAG	840
Db	781	GTCTCGCGGCTGTGTGGCGCGTGGTCTGTCTTTCGCGCGCTGTCTGGGCCCCCATCCAG	840
Qy	841	CTGTTCTCTGGTCTGCAGGGCGCTGGGCCCCCGCGGGCTCCTGGCACCCACGCAAGTACGCC	900
Db	841	CTGTTCTCTGGTCTGCAGGGCGCTGGGCCCCCGCGGGCTCCTGGCACCCACGCAAGTACGCC	900
Qy	901	GCCTACGCGCTTAAGAAGCTGGGCTCACTGCATGTCTTACAGCAACTCCGGGCTGAAACCGC	960
Db	901	GCCTACGCGCTTAAGAAGCTGGGCTCACTGCATGTCTTACAGCAACTCCGGGCTGAAACCGC	960
Qy	961	CTGCTCTACGCTTCTGGGCTCGCACTTTCGACAGAGGCTTTCGCGCGCTGTGCCCTGTC	1020
Db	961	CTGCTCTACGCTTCTGGGCTCGCACTTTCGACAGAGGCTTTCGCGCGCTGTGCCCTGTC	1020
Qy	1021	GCGCGCGCGCGCCCCCGCGCCCCCGCGGCCCGGACCTCTCGACCCCGCGAGCCCCACAC	1080
Db	1021	GCGCGCGCGCGCCCCCGCGCCCCCGCGGCCCGGACCTCTCGACCCCGCGAGCCCCACAC	1080
Qy	1081	GCGAGCTGTGACCGCCTGGGCTCCACCCCGCCCCCGCGAGGGCGCAGAGCCAGGGAGC	1140
Db	1081	GCGAGCTGTGACCGCCTGGGCTCCACCCCGCCCCCGCGAGGGCGCAGAGCCAGGGAGC	1140
Qy	1141	AGTGGGCTGGCCGCGCGGCTGTGCGTCTTGGGGAGGACAAACGCCCTCTCTCTGA	1197
Db	1141	AGTGGGCTGGCCGCGCGGCTGTGCGTCTTGGGGAGGACAAACGCCCTCTCTCTGA	1197

RESULT 2

US-10-295-027-747
; Sequence 747, Application US/10295027

Publication No. US20030232350A1
GENERAL INFORMATION:

APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

APPLICANT: Ginsberg, We

;; APPLICANT: GIBB, KURT C
;; APPLICANT: Glynne, Rich

APPLICANT: Hevezi, Peter A.

QY 1 ATGCACCGCTGGCTACGTCGGACCCAAACGGTCTCTGGGGGGACACGGCCAAACGCCTCC 60
Db |||||
1 ATGCACACCGTGGCTACGTCGGACCCAAACGGTCTCTGGGGGGACACGGCCAAACGCCTCC 60
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Db |||||
61 GGTCTCCCGGGGTGTGGGGCCAAACGCCCTCGACAGCCCAAGTCCCTTCGCCCGGGCCGGTG 120
QY 121 GACCGCTGGCTGTGGCGCTCTTCTTCGCCGGCGCTGATGCTGCTGGGGCTGTGGGGAAC 180
Db |||||
121 GACCGCTGGCTGTGGCGCTCTTCTTCGCCGGCGCTGATGCTGCTGGGGCTGTGGGGAAC 180
QY 181 TCGCTGTCATCTAGTCTGCGCGCCACAGCCGATGCGGACCGTGAACACTTCTAC 240
Db |||||
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QY 241 ATCGCCAACTTGGCGGCCACGGACGTGACCTTCTCTGCTGGTCCCTTCAACGCC 300
Db |||||
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QY 301 CTGCTGTACCCGCTGCCCGGTGGTGTGGCGACTTCTCTGCTGGTCCCTTCAACACTAC 360
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301 CTGCTGTACCCGCTGCCCGGTGGTGTGGCGACTTCTCTGCTGGTCCCTTCAACACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGAGGCCACAGTGTGCCACTCTGACGGCCATGAGTGTGGACGC 420
Db |||||
361 ATCCAGCAGGTCTCGGTGAGGCCACAGTGTGCCACTCTGACGGCCATGAGTGTGGACGC 420
QY 421 TGGTACGTGAGGTGTCCGCTTGGCGCCCTGACCGCCGACCGCCGCTGGCGGTG 480
Db |||||
421 TGGTACGTGAGGTGTCCGCTTGGCGCCCTGACCGCCGACCGCCGCTGGCGGTG 480
QY 481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGGGGTCTGCGCGGTG 540
Db |||||
481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGGGGTCTGCGCGGTG 540
QY 541 CACCGCTGTACCCGGGGCGCGCCCTACTGCACTGAGTGGGCTTCTCCCGAGCGCGCCGTG 600
Db |||||
541 CACCGCTGTACCCGGGGCGCGCCCTACTGCACTGAGTGGGCTTCTCCCGAGCGCGCCGTG 600
QY 601 GAGCGCGCTTTCGCACTGTAAACCTGCTGGCGCTGTACTGCTGCTGCCCTGCTGCCACC 660
Db |||||
601 GAGCGCGCTTTCGCACTGTAAACCTGCTGGCGCTGTACTGCTGCTGCCCTGCTGCCACC 660
QY 661 TCGCGCTGTATGCGGCCATGCTGGCCACCTGGGCGGGTGTGCGTGGCGCCCGCGCC 720
Db |||||
661 TCGCGCTGTATGCGGCCATGCTGGCCACCTGGGCGGGTGTGCGTGGCGCCCGCGCC 720
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Db |||||
721 GCCGATAGCGCCCTGACGGGGCAGGTGTGGCAGAGCGGACGGCGCGTGGGGCCAAAG 780
QY 781 GTCTCGCGCTGTGGCGCGTGTCTGCTTTCGCGCGCTGCTGGGGGCCCATCCAG 840
Db |||||
781 GTCTCGCGCTGTGGCGCGTGTCTGCTTTCGCGCGCTGCTGGGGGCCCATCCAG 840
QY 841 CTGTTCTGTGTGCTGACGGCGTGGGGCCCGGGCTCTCTGGACCCACGACGACTAGGCC 900
Db |||||
841 CTGTTCTGTGTGCTGACGGCGTGGGGCCCGGGCTCTCTGGACCCACGACGACTAGGCC 900
QY 901 GCCTACGGCGCTTAAGACTGGGCTCACTGCACTGCTTACAGCACTCCGCGCTGAACCCG 960
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901 GCCTACGGCGCTTAAGACTGGGCTCACTGCACTGCTTACAGCACTCCGCGCTGAACCCG 960
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Db |||||
961 CTGCTCTACGCTTCTCTGGGTGCACTTTCGACAGGCTTTCGCGCGGTCTGCCCTTGC 1020
QY 1021 GCGCGCGCGCGCCCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db |||||
1021 GCGCGCGCGCGCCCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
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Db 1081 GCGGAGCTGCACCGCTGGGGTCCACCCGGGGCCCCCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 AGTGGCTGGCGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCCCTCTCTGA 1197
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1141 AGTGGCTGGCGCGCGCGCGCGCTGTGCTCTCTGGGGGAGGACAAACGCCCTCTCTGA 1197
RESULT 7
US-09-796-338A-18
; Sequence 18, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796.338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-338A-18
Query Match 99.9%; Score 1195.4; DB 3; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 61 GGTCTCCCGGGGTGTGGGGCCAAACGCCCTCGACAGCCCAAGTCCCTTCGCCCGGGCCGGTG 120
Db |||||
61 GGTCTCCCGGGGTGTGGGGCCAAACGCCCTCGACAGCCCAAGTCCCTTCGCCCGGGCCGGTG 120
QY 121 GACCGCTGGCTGTGGCGCTCTTCTTCGCCGGCGCTGATGCTGCTGGGGCTGTGGGGAAC 180
Db |||||
121 GACCGCTGGCTGTGGCGCTCTTCTTCGCCGGCGCTGATGCTGCTGGGGCTGTGGGGAAC 180
QY 181 TCGCTGTCATCTAGTCTGCGCGCCACAGCCGATGCGGACCGTGAACACTTCTAC 240
Db |||||
181 TCGCTGTCATCTAGTCTGCGCGCCACAGCCGATGCGGACCGTGAACACTTCTAC 240
QY 241 ATCGCCAACTTGGCGGCCACGGACGTGACCTTCTCTGCTGGTCCCTTCAACGCC 300
Db |||||
241 ATCGCCAACTTGGCGGCCACGGACGTGACCTTCTCTGCTGGTCCCTTCAACGCC 300
QY 301 CTGCTGTACCCGCTGCCCGGTGGTGTGGCGACTTCTCTGCTGGTCCCTTCAACACTAC 360
Db |||||
301 CTGCTGTACCCGCTGCCCGGTGGTGTGGCGACTTCTCTGCTGGTCCCTTCAACACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGAGGCCACAGTGTGCCACTCTGACGGCCATGAGTGTGGACGC 420
Db |||||
361 ATCCAGCAGGTCTCGGTGAGGCCACAGTGTGCCACTCTGACGGCCATGAGTGTGGACGC 420
QY 421 TGGTACGTGAGGTGTCCGCTTGGCGCCCTGACCGCCGACCGCCGCTGGCGGTG 480
Db |||||
421 TGGTACGTGAGGTGTCCGCTTGGCGCCCTGACCGCCGACCGCCGCTGGCGGTG 480
QY 481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGGGGTCTGCGCGGTG 540
Db |||||
481 GCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGGGGTGTCTGCGGGGTCTGCGCGGTG 540
QY 541 CACCGCTGTACCCGGGGCGCGCCCTACTGCACTGAGTGGGCTTCTCCCGAGCGCGCCGTG 600
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541 CACCGCTGTACCCGGGGCGCGCCCTACTGCACTGAGTGGGCTTCTCCCGAGCGCGCCGTG 600

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DB 601 GAGCGCGCTTCGACCTGTACAACTGTGGCGCTGTACCTGTCTGCGCTGTGCGCAAC 660
QY 661 TCGCGCTGTATGCGCGCATGTGCGCACCTGCGCGCGGTGCGCTGCGCGCGCGCG 720
DB 661 TCGCGCTGTATGCGCGCATGTGCGCACCTGCGCGCGGTGCGCTGCGCGCGCGCG 720
QY 721 GCCGATAGCGCGCTGCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGCGCAAG 780
DB 721 GCCGATAGCGCGCTGCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGCGCAAG 780
QY 781 GTCTCGCGCTGTGCGCGCATGTGCGCTGTGCGCGCTGTGCGCGCTGTGCGCGCTGTGCGCG 840
DB 781 GTCTCGCGCTGTGCGCGCATGTGCGCTGTGCGCGCTGTGCGCGCTGTGCGCGCTGTGCGCG 840
QY 841 CTGTTCTCTGCTGCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 900
DB 841 CTGTTCTCTGCTGCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 900
QY 901 GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCTACAGCAACTCCGCGCTGAACCGG 960
DB 901 GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCTACAGCAACTCCGCGCTGAACCGG 960
QY 961 CTGCTCTACGCTTCTGCGCTGCGCATCTTCCGACAGGCTTCCGCGCGCTGCGCGCTGCG 1020
DB 961 CTGCTCTACGCTTCTGCGCTGCGCATCTTCCGACAGGCTTCCGCGCGCTGCGCGCTGCG 1020
QY 1021 GCG 1080
DB 1021 GCG 1080
QY 1081 GCGGAGCTGACAGCGCTGGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 GCGGAGCTGACAGCGCTGGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGCTGTGCGGGGAGGACAAACCGCCCTCTCTGA 1197
DB 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGCTGTGCGGGGAGGACAAACCGCCCTCTCTGA 1197

RESULT 8

US-09-897-201-1
; Sequence 1, Application US/09897201
; Patent No. US20020077469A1
; GENERAL INFORMATION:
; APPLICANT: BOROMSKY, BETH E
; APPLICANT: QUAN, YONG
; APPLICANT: SMITH, KELI E
; TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF 11 RECEPTOR
; FILE REFERENCE: 1795/58800a
; CURRENT APPLICATION NUMBER: US/09/897,201
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/266,127
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-897-201-1

Query Match 99.9%; Score 1195.4; DB 3; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTACGTCGGACCCAAACGGTCTCTGGGGGCGACCGCGCAACCGCTCC 60
DB 1 ATGCACACCGTGGCTACGTCGGACCCAAACGGTCTCTGGGGGCGACCGCGCAACCGCTCC 60
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DB 181 TCGCTGGTCACTTACGTCACTGCGCGCACAGCCGATGCGGACCGTGAACCAACTTCTAC 240
QY 241 ATCGCAACCTGCGCGCACAGGACGTGACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 ATCGCAACCTGCGCGCACAGGACGTGACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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DB 301 CTGCTGTACCGCTGCGCGCTGGGCTGCTGGGCGACTTCTATGTCAAGTTCTGCTCAACTAC 360
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DB 361 ATCCAGCAGGTCTCGGTGACGCGCACGTGTGCCACTCTCTGACCGCATGAGTGTGACCGC 420
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DB 481 GCTGTACGCTGACGCTGCTGCGCGCTGGGCTGCTGGGCGGTCTGCGCGCGGTCTGCGCGCTG 540
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DB 601 GAGCGCGCTTTCGACCTGTGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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DB 661 TCGCGCTGTATGCGCGCATGCTGCGCGCTGGGCTGCTGGGCGGTGCTGCGCGCGGTGCTG 720
QY 721 GCCGATAGCGCGCTTTCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGCGCAAG 780
DB 721 GCCGATAGCGCGCTTTCGAGGGGAGGTGTGCGCAGAGCGCGCAGGGCGCGCTGCGCGCAAG 780
QY 781 GTCTCGCGCTGTGCTGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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DB 841 CTGTTCTCTGCTGCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 900
QY 901 GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCTACAGCAACTCCGCGCTGAACCGG 960
DB 901 GCCTACGCGCTTAAGACCTGGGCTCACTGATGTCTACAGCAACTCCGCGCTGAACCGG 960
QY 961 CTGCTCTACGCTTCTGCGCTGCGCATCTTCCGACAGGCTTCCGCGCGCTGCGCGCTGCG 1020
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DB 1021 GCG 1080
QY 1081 GCGGAGCTGACAGCGCTGGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
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QY 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGCTGTGCGGGGAGGACAAACCGCCCTCTCTGA 1197
DB 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGCTGTGCGGGGAGGACAAACCGCCCTCTCTGA 1197

121 GAGCGCTGGCTGGTGGCGCTCTTTCTTCGCGCGCTGATCTCTCTGGCGCTGGTGGGAC 180
181 TGGCTGGTCACTACGTCATCTGCGCCCAAGCCGATCGGACCGTGACCAACTTCTAC 240
181 TGGCTGGTCACTACGTCATCTGCGCCCAAGCCGATCGGACCGTGACCAACTTCTAC 240
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421 TGGTACGTGACGCTGTTCCGTTGGCGGCTGCGGCTGCGACCGCGCGCTGGCGCTG 480
421 TGGTACGTGACGCTGTTCCGTTGGCGGCTGCGGCTGCGACCGCGCGCTGGCGCTG 480
481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGCTGCTGCGCGGCTGCTGCGCG 540
481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGCTGCTGCGCGGCTGCTGCGCG 540
541 CACCGCTGTACCGCGCGCGCGCTTACGAGTGGGCTTCCCGAGCGCGCGCTG 600
541 CACCGCTGTACCGCGCGCGCGCTTACGAGTGGGCTTCCCGAGCGCGCGCTG 600
601 GAGCGCGCTTCGCACTGTAACCTGTGCGGCTGTAACCTGTGCGCTGCTGCGCAAC 660
601 GAGCGCGCTTCGCACTGTAACCTGTGCGGCTGTAACCTGTGCGCTGCTGCGCAAC 660
661 TGGCGCTGTATGCGGCCATGCTGCGGCCACTTGGCGCGGCTGCGCGCGCGCGCG 720
661 TGGCGCTGTATGCGGCCATGCTGCGGCCACTTGGCGCGGCTGCGCGCGCGCGCG 720
721 GCGGATAGCGGCTGCGAGGCGAGGCTGCGGAGAGCGCGAGGCGCGGCGCGCGCG 780
721 GCGGATAGCGGCTGCGAGGCGAGGCTGCGGAGAGCGCGAGGCGCGGCGCGCGCG 780
781 GTCTCGCGCTGGTGGCGCGCTGCTCTGCTCTTTCGCGCGCTGCTGGGCGCGCAATCCAG 840
781 GTCTCGCGCTGGTGGCGCGCTGCTCTGCTCTTTCGCGCGCTGCTGGGCGCGCAATCCAG 840
841 CTGTTCTTGGTGTGAGCGCTGGGCGCGCGCGCGCGCGCTGCGCAATCCAGCGCTACGCG 900
841 CTGTTCTTGGTGTGAGCGCTGGGCGCGCGCGCGCGCGCTGCGCAATCCAGCGCTACGCG 900
901 GCTTACGCGCTTAAAGACCTGGGCTCACTGCAATGCTTACAGCAATCCGCGCTGAAACCG 960
901 GCTTACGCGCTTAAAGACCTGGGCTCACTGCAATGCTTACAGCAATCCGCGCTGAAACCG 960
961 CTGCTCTACGCTTCTGGGCTCGCACTTCCGACAGGCTTCCGCGCGCTGCGCGCTGCG 1020
961 CTGCTCTACGCTTCTGGGCTCGCACTTCCGACAGGCTTCCGCGCGCTGCGCGCTGCG 1020
1021 GCG 1080
1021 GCG 1080
1081 GCGGAGCTGACCGCTGGGCTGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
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1141 AGTGGGCTGGCGCGCGCGCTGTCGCTGCGGCGGAGCAACCGCGCTCTCTGA 1197

US-10-145-586-18
; Sequence 18, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silvio-Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-145-586-18

Query Match 99.9%; Score 1195.4; DB 6; Length 1197;
Best Local Similarity 99.9%; Pred. No. 6.6e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTACGTCGCGGACCCCAACGCGTCTCTGGGGGGCACCGGCAACGCTCC 60
Db 1 ATGCACACCGTGGCTACGTCGCGGCCCCAACGCGTCTCTGGGGGGCACCGGCAACGCTCC 60
QY 61 GGCTGCCCGGGCTGTGGCGCAACGCTTCGAGCGGCCAGTCCCTTCGCGCGGGCGGTG 120
Db 61 GGCTGCCCGGGCTGTGGCGCAACGCTTCGAGCGGCCAGTCCCTTCGCGCGGGCGGTG 120
QY 121 GACGCTGGCTGCTGCGCTCTTCTTCGCGGCGCTGATGCTGCTGGGCTGGTGGGGAAC 180
Db 121 GACGCTGGCTGCTGCGCTCTTCTTCGCGGCGCTGATGCTGCTGGGCTGGTGGGGAAC 180
QY 181 TCGCTGGTCACTACGTCACTGCGGCCACAAAGCCGATGCGGACCGTGACCAACTTCTAC 240
Db 181 TCGCTGGTCACTACGTCACTGCGGCCACAAAGCCGATGCGGACCGTGACCAACTTCTAC 240
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Db 241 ATCGCAACCTGGGGGCCACGAGCGTACCTTCTCTGCTGGTCCCTTTCACGCGCC 300
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Db 301 CTGCTGTACCGCTGCGCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 360
QY 361 ATCCAGCAGGCTCTGGTGCAGGCCACGCTGCGCACTCTGACCGCATGAGTGTGACGCGC 420
Db 361 ATCCAGCAGGCTCTGGTGCAGGCCACGCTGCGCACTCTGACCGCATGAGTGTGACGCGC 420
QY 421 TGGTACGTGACGCTGTTCCCGTTGGCGGCTGCGCAACCGCGCGCGCGCGCTGGCGCTG 480
Db 421 TGGTACGTGACGCTGTTCCCGTTGGCGGCTGCGCAACCGCGCGCGCGCGCTGGCGCTG 480
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGCTGCTGCGCGGCTGCTGCGCGCTG 540
Db 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGCTGCTGCGCGGCTGCTGCGCGCTG 540
QY 541 CACCGCTGTCAACCGGGCGCGCGCTTACGAGTGGGCTTCCCGAGCGCGCGCGCGCTG 600
Db 541 CACCGCTGTCAACCGGGCGCGCGCTTACGAGTGGGCTTCCCGAGCGCGCGCGCGCTG 600
QY 601 GAGCGCGCTTCGCACTGTAACCTGTGCGGCTGTAACCTGTGCGCTGCTGCGCAAC 660
Db 601 GAGCGCGCTTCGCACTGTAACCTGTGCGGCTGTAACCTGTGCGCTGCTGCGCAAC 660

[illegible]

RESULT 13

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RES001.13
US-09-796-338A-16
; Sequence 16, Application US/09796338A
; Patent No. US2002061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 43449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796.338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)...(1369)
US-09-796-338A-16

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RESULT 14

RESUL 14
 US-10-282-837-16
 ; Sequence 16, Application US/10282837
 ; Publication No. US20030082738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
 ; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
 ; FILE REFERENCE: 10448-020001
 ; CURRENT APPLICATION NUMBER: US/10/282,837
 ; CURRENT FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: US/09/796,338
 ; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)...(1369)
US-10-282-837-16

Query Match 99.9%; Score 1195.4; DB 5; Length 1609;

Best Local Similarity 99.9%; Pred. No. 6.3e-246;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ATGCACACCGTGGCTACGTCGCGACCCAAACGCTCTCGGGGGGACCGGCGCAACGCGCTCC 60
Db 176 ATGCACACCGTGGCTACGTCGCGGCGCCAAACGCGTCTCGGGGGGACCGGCGCAACGCGCTCC 235
Qy 61 GCGTCCCGGGCTGTGGGCGCAACGCTCGGACGGCCCGAGTCCCTTCGCCCGCGGGCGGTG 120
Db 236 GCGTCCCGGGCTGTGGGCGCAACGCTCGGACGGCCCGAGTCCCTTCGCCCGCGGGCGGTG 295
Qy 121 GACGCTCGGCTGTGGCGGCTCTTCTTCGGGGGCTGATGCTGCTGGGCTGTGGGGAAC 180
Db 296 GACGCTCGGCTGTGGCGGCTCTTCTTCGGGGGCTGATGCTGCTGGGCTGTGGGGAAC 355
Qy 181 TCGCTGTGTCATCTAGCTACGTCGCGACCGCATCGCGACCGCGATCGCGACCGCGCTGCTG 240
Db 356 TCGCTGTGTCATCTAGCTACGTCGCGGCGCCAAACGCTCGGACCGCGATCGCGACCGCGCTGCTG 415
Qy 241 ATGCGCAACCTGGGCGGCGACGGAAGTACCTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 416 ATGCGCAACCTGGGCGGCGACGGAAGTACCTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
Qy 301 CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCGACTTCATGTCGAAGTGTGCTCAACTAC 360
Db 476 CTGCTGTACCGCTGCGCGGCTGGGTGCTGGGCGACTTCATGTCGAAGTGTGCTCAACTAC 535
Qy 361 ATCCAGAGGTCTCGGTGACGCGACGCTGTCGCACTCTGACCGCGCATGAGTGTGACCGCG 420
Db 536 ATCCAGAGGTCTCGGTGACGCGACGCTGTCGCACTCTGACCGCGCATGAGTGTGACCGCG 595
Qy 421 TGGTACGTGACGGGTTCCTCGGTGCGCGCTTGCACCGCGCGACCGCGCGCTGCGCGCTG 480
Db 596 TGGTACGTGACGGGTTCCTCGGTGCGCGCTTGCACCGCGCGACCGCGCGCTGCGCGCTG 655
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGGGCTGCTGCGCGGCTGCTGCGCGCTG 540
Db 656 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGGGCTGCTGCGCGGCTGCTGCGCGCTG 715
Qy 541 CACGCGCTGTACCGCGGCGCGCGCTTACGTCAGTGAAGCTTCCCGACGCGCGCGCTG 600
Db 716 CACGCGCTGTACCGCGGCGCGCGCTTACGTCAGTGAAGCTTCCCGACGCGCGCGCTG 775
Qy 601 GAGCGCGCTTTCGCACTGTACAACCTGTGCGGCTGTACCTGTGCTGCTGCTGCTGCTGCTG 660
Db 776 GAGCGCGCTTTCGCACTGTACAACCTGTGCGGCTGTACCTGTGCTGCTGCTGCTGCTGCTG 835
Qy 661 TGGCGCTGTATGCGGCGCATGCTGGCGCACCTGGGCGGGGTGCGGTGCGGCGCGCGCGCTG 720
Db 836 TGGCGCTGTATGCGGCGCATGCTGGCGCACCTGGGCGGGGTGCGGTGCGGCGCGCGCGCTG 895
Qy 721 GCCGATAGCGGCTTTCAGGGGAGGTGTGTCAGAGCGCGACGCGCGCGCTGCGGGCGCAAG 780
Db 896 GCCGATAGCGGCTTTCAGGGGAGGTGTGTCAGAGCGCGACGCGCGCGCTGCGGGCGCAAG 955
Qy 781 GTCTCGCGGCTGTGGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 956 GTCTCGCGGCTGTGGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
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Qy 841 CTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 1016 CTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
Qy 901 GCCTACGCGCTTAAAGACTCTGGGCTCACTGCAATGCTTACAGCAACTCTCGCGCTGAACCCG 960
Db 1076 GCCTACGCGCTTAAAGACTCTGGGCTCACTGCAATGCTTACAGCAACTCTCGCGCTGAACCCG 1135
Qy 961 CTGCTCTACGCGCTTCTGCGGCTCGCACTTTCGACAGAGCTTTCGCGCGCTGCTGCGCGCTG 1020
Db 1136 CTGCTCTACGCGCTTCTGCGGCTCGCACTTTCGACAGAGCTTTCGCGCGCTGCTGCGCGCTG 1195
Qy 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
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Qy 1141 AGTGGGCTGCGCGCGCGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
Db 1316 AGTGGGCTGCGCGCGCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1372
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RESULT 15

US-10-145-586-16

; Sequence 16, Application US/10145586

; Publication No. US20030138890A1

; GENERAL INFORMATION:

; APPLICANT: Alexandra Gluckmann, Maria

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: M. Galvin, Katherine

; APPLICANT: Weich, Nadine

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Bandaru, Rajasekhar

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,

; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

; FILE REFERENCE: 10448-188001

; CURRENT APPLICATION NUMBER: US/10/145,586

; CURRENT FILING DATE: 2002-05-14

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 1609

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (176)...(1369)

US-10-145-586-16

Query Match 99.9%; Score 1195.4; DB 6; Length 1609;

Best Local Similarity 99.9%; Pred. No. 6.3e-246;

Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ATGCACACCGTGGCTACGTCGCGACCCAAACGCTCTCGGGGGGACCGGCGCAACGCGCTCC 60
Db 176 ATGCACACCGTGGCTACGTCGCGGCGCCAAACGCTCTCGGGGGGACCGGCGCAACGCGCTCC 235
Qy 61 GCGTCCCGGGCTGTGGGCGCAACGCTCGGACGGCCCGAGTCCCTTCGCCCGCGGGCGGTG 120
Db 236 GCGTCCCGGGCTGTGGGCGCAACGCTCGGACGGCCCGAGTCCCTTCGCCCGCGGGCGGTG 295
Qy 121 GACGCTCGGCTGTGGCGGCTCTTCTTCGGGGGCTGATGCTGCTGGGCTGTGGGGAAC 180
Db 296 GACGCTCGGCTGTGGCGGCTCTTCTTCGGGGGCTGATGCTGCTGGGCTGTGGGGAAC 355
Qy 181 TCGCTGTGTCATCTAGCTACGTCATCTGCGGCGCAACGCGCGATGCGGACCGTCAACTTCAC 240
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Db 356 TCCTGGTCACTACGTCACTCCGCCACAAGCCGATGCGGACCGTGACCAACTTCTAC 415
 QY 241 ATCGCAACCTGGCGGCCACGACGTGACCTTCTCTGTGTGCTGCGTCCCTTTCACGGCC 300
 Db 416 ATCGCAACCTGGCGGCCACGACGTGACCTTCTCTGTGTGCTGCGTCCCTTTCACGGCC 475
 QY 301 CTGCTGTACCCGCTGCGCGCTGGGTGCTGGGCGAATTATGTGCAAGTTGCTCAACTAC 360
 Db 476 CTGCTGTACCCGCTGCGCGCTGGGTGCTGGGCGAATTATGTGCAAGTTGCTCAACTAC 535
 QY 361 ATCCAGCAGGTCTCGGTGAGGGCAGGTGTGCCACTCTGACCGCCATGAGTGTGGACCGC 420
 Db 536 ATCCAGCAGGTCTCGGTGAGGGCAGGTGTGCCACTCTGACCGCCATGAGTGTGGACCGC 595
 QY 421 TGGTACGTGACGGTGTTCGGCTTGGCGGCTTACCGCGCAGCGCCCGCTGGGGCTG 480
 Db 596 TGGTACGTGACGGTGTTCGGCTTGGCGGCTTACCGCGCAGCGCCCGCTGGGGCTG 655
 QY 481 GCTGTACGGCTTACGACATCTGGGTAGGCTCTGGGGCGGTGTCTGCGCGGTGCTGCGCCCTG 540
 Db 656 GCTGTACGGCTTACGACATCTGGGTAGGCTCTGCGCGGTGCTGCGCGGTGCTGCGCCCTG 715
 QY 541 CACCGGCTGTACCGCGGCGCGGCTTACGAGTGAGGCTTCCCGAGCGCGCGCTG 600
 Db 716 CACCGGCTGTACCGCGGCGCGGCTTACGAGTGAGGCTTCCCGAGCGCGCGCTG 775
 QY 601 GAGCGGCTTTCGACCTGTACAACTGTGGGCTGTACTGTGCGCGTGTCTGCGCAC 660
 Db 776 GAGCGGCTTTCGACCTGTACAACTGTGGGCTGTACTGTGCGCGTGTCTGCGCAC 835
 QY 661 TGGCGCTGTATGCGGCCATGTGCGCCACTTGGGCGGGTCTGCGTGGCGCGCGCC 720
 Db 836 TGGCGCTGTATGCGGCCATGTGCGCCACTTGGGCGGGTCTGCGTGGCGCGCGCC 895
 QY 721 GCGGATAGCGCTTACGGGCGAGGTGTGCGAGAGCGCGCAGGCGCGTGTGGGCGCAAG 780
 Db 896 GCGGATAGCGCTTACGGGCGAGGTGTGCGAGAGCGCGCAGGCGCGTGTGGGCGCAAG 955
 QY 781 GTCTCGCGGCTGTGGCGCGCGTGTGCTCTTCCGCGCGCTGTGGGCGCGCATCCAG 840
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 Db 1016 CTGTTCTGTGTGTCAGGCGCTGGGCGCGCGGCTCTTGGCACCCACGACGCTACGCC 1075
 QY 901 GCCTAGCGGCTTAAAGACCTGGGCTCACTGCGATGTCTACAGCAACTCCGCGCTGAACCG 960
 Db 1076 GCCTAGCGGCTTAAAGACCTGGGCTCACTGCGATGTCTACAGCAACTCCGCGCTGAACCG 1135
 QY 961 CTGCTCTAGCGCTTCTGGGCTCGCACTTCCGACAGGCTTCCGCGGCTGTGGCGCGCTGC 1020
 Db 1136 CTGCTCTAGCGCTTCTGGGCTCGCACTTCCGACAGGCTTCCGCGGCTGTGGCGCGCTGC 1195
 QY 1021 GCG 1080
 Db 1196 GCG 1255
 QY 1081 GCGGAGCTGACGCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 1140
 Db 1256 GCGGAGCTGACGCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 1315
 QY 1141 AGTGGGCTGCG 1197
 Db 1316 AGTGGGCTGCG 1372

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM nucleic - nucleic search, using sw model

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(without alignments)
8311.489 Million cell updates/sec

Title: US-10-771-417-6
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Searched: 1303057 seqs, 888780828 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	187.8	15.7	1219	3	US-08-981-700A-3
4	186.8	15.6	1365	3	US-08-999-112B-27
5	186.8	15.6	1365	3	US-09-011-553-4
6	186.2	15.6	1164	3	US-08-993-088A-6
7	186.2	15.6	1164	3	US-08-993-424B-6
8	186.2	15.6	1164	3	US-09-603-680-6
9	184.6	15.4	1164	3	US-09-826-509-504
10	175	14.6	1296	2	US-07-816-283-9
11	175	14.6	1296	2	US-08-417-103-9
12	175	14.6	1413	3	US-09-016-434-1321
13	173.4	14.5	1257	3	US-08-926-509-572
14	171.2	14.3	1047	3	US-08-540-650B-6
15	171.2	14.3	1050	3	US-09-826-509-502
16	171.2	14.3	1053	3	US-09-016-434-1423
17	171.2	14.3	1882	3	US-08-540-650B-11
18	171.2	14.3	3083	3	US-08-693-308-1
19	168	14.0	1107	3	US-09-595-549-3
20	168	14.0	1417	3	US-09-199-737-3
21	168	14.0	1417	3	US-09-058-333A-3
22	163.2	13.6	1796	2	US-07-816-283-11
23	163.2	13.6	1796	2	US-08-417-103-11
24	158.4	13.2	1275	3	US-08-916-247A-3

25	149.4	12.5	1690	3	US-08-665-034A-1	Sequence 1, Appli
26	148.2	12.4	1193	3	US-08-899-112B-7	Sequence 7, Appli
27	148.2	12.4	1193	3	US-09-011-553-1	Sequence 1, Appli
28	148.2	12.4	1714	3	US-08-981-700A-1	Sequence 1, Appli
29	146.6	12.2	1116	3	US-08-993-088A-18	Sequence 18, Appli
30	146.6	12.2	1116	3	US-08-993-424B-18	Sequence 18, Appli
31	146.6	12.2	1116	3	US-09-603-680-18	Sequence 18, Appli
32	146.6	12.2	1119	2	US-08-626-685A-7	Sequence 7, Appli
33	145.4	12.1	1607	3	US-08-540-650B-17	Sequence 17, Appli
34	145	12.1	1116	3	US-08-993-088A-19	Sequence 19, Appli
35	145	12.1	1116	3	US-09-603-680-19	Sequence 19, Appli
36	144	12.0	1280	3	US-09-199-737-1	Sequence 1, Appli
37	144	12.0	1280	3	US-08-900-230-1	Sequence 1, Appli
38	144	12.0	1280	3	US-09-058-333A-1	Sequence 1, Appli
39	142.2	11.9	1044	3	US-08-513-974B-47	Sequence 47, Appli
40	142.2	11.9	1044	3	US-08-540-650B-4	Sequence 4, Appli
41	142.2	11.9	1044	3	US-09-461-436B-47	Sequence 47, Appli
42	142.2	11.9	1607	3	US-08-513-974B-341	Sequence 341, App
43	141.4	11.8	1167	3	US-08-826-509-574	Sequence 574, App
44	141.4	11.8	1317	3	US-09-016-434-1446	Sequence 1446, Ap
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ALIGNMENTS

RESULT 1

US-09-830-428A-6
; Sequence 6, Application US/09830428A
; Patent No. 6699965

GENERAL INFORMATION:

; APPLICANT: Takuya WATANABE
; APPLICANT: Yasuko TERAOKA
; APPLICANT: Yasushi SHINTANI
; APPLICANT: Tetsuya OHTAKI
; APPLICANT: Kimiko KANEHASHI
; APPLICANT: Chieko KITADA
; TITLE OF INVENTION: No. 6699965el G Protein Coupled Receptor Protein, DNA and its Lig
; FILE REFERENCE: 2001-0272A/WMC/01801
; CURRENT APPLICATION NUMBER: US/09/830,428A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 10-305949
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: JP 11-027710
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: JP 11-057207
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: JP 11-276225
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 22

SEQ ID NO 6

LENGTH: 1197

TYPE: DNA

ORGANISM: Human

US-09-830-428A-6

Query Match 100.0%; Score 1197; DB 3; Length 1197;
Best Local Similarity 100.0%; Pred. No. 3.1e-180;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCACACCGTGGCTACGTCGACCCACCGCTCTCGGGGGCCACCGGCCACGCTCC	60
Db	1	ATGCACACCGTGGCTACGTCGACCCACCGCTCTCGGGGGCCACCGGCCACGCTCC	60
Qy	61	GGCTGCCCGGGCTGTGGCGCCCAACGCTCGACGGCCAGTCCCTTCGCGCGGGGCGGTG	120
Db	61	GGCTGCCCGGGCTGTGGCGCCCAACGCTCGACGGCCAGTCCCTTCGCGCGGGGCGGTG	120
Qy	121	GACGCTTGGCTCGTGCCTCTTCTTCGCGCGCTGATGCTGTGGGCTGTGGGGAAC	180
Db	121	GACGCTTGGCTCGTGCCTCTTCTTCGCGCGCTGATGCTGTGGGCTGTGGGGAAC	180
Qy	181	TGCTGGTTCATCTACGTCTATCTGCCGCCACAGCGATCGGACCGTGCACCACTTCTAC	240

Db TCCTGGTCACTACGTCATCTGCGCCACAAGCGATGCGGACCGTGACCAACTTCTAC 240
Qy ATCCGCAACCTGGCGCCACGAGCTGACCTTCTCTGTGCTGGTCCCTTCACGCC 300
Db ATCGCAACCTGGCGGCCACGAGCTGACCTTCTCTGTGCTGGTCCCTTCACGCC 300
Qy CTGTGTACCCGCTGCCCGGCTGGGTGCTGGCGACTTCATGTGCAAGTTCGTAACATAC 360
Db CTGTGTACCCGCTGCCCGGCTGGGTGCTGGCGACTTCATGTGCAAGTTCGTAACATAC 360
Qy ATCCAGCAGGTCTCGGTGCAAGCCACGCTGTCCTACTGTGACCGCATGAGTGTGAGCCGC 420
Db ATCCAGCAGGTCTCGGTGCAAGCCACGCTGTCCTACTGTGACCGCATGAGTGTGAGCCGC 420
Qy TGTACGTGAGGTGTTCCCGTGGCGCCCTGACCGCCGACCGCCCGCTGGCGTG 480
Db TGTACGTGAGGTGTTCCCGTGGCGCCCTGACCGCCGACCGCCCGCTGGCGTG 480
Qy GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGGCGGGTCTGCCCTG 540
Db GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGGCGGGTCTGCCCTG 540
Qy CACCGCTGTCAACCGGCGCGCGCTTACTGCAAGTGGGCTTCCCGAGCGCGCCCTG 600
Db CACCGCTGTCAACCGGCGCGCGCTTACTGCAAGTGGGCTTCCCGAGCGCGCCCTG 600
Qy GAGCGGCTTGCNACTGTAACCTGCTGGCGCTGACCTGCTGGCGCTGCTGCCACC 660
Db GAGCGGCTTGCNACTGTAACCTGCTGGCGCTGACCTGCTGGCGCTGCTGCCACC 660
Qy TGGCGCTGTATGGCCCATGCTGGCCCATCTGGCCGGGTGCGCTGGCGCCGCGCC 720
Db TGGCGCTGTATGGCCCATGCTGGCCCATCTGGCCGGGTGCGCTGGCGCCGCGCC 720
Qy GCCGATAGCGCCCTGCAAGGCGAGGTGTGCGAGAGCGCGAGCGCGCGCGGCGCAAG 780
Db GCCGATAGCGCCCTGCAAGGCGAGGTGTGCGAGAGCGCGAGCGCGCGCGGCGCAAG 780
Qy GTCTCGCGCTGGTGGCGCGGTGCTGCTCTTCGCGCGCTGCTGGGCGCCATCCAG 840
Db GTCTCGCGCTGGTGGCGCGGTGCTGCTCTTCGCGCGCTGCTGGGCGCCATCCAG 840
Qy CTGTTCTCTGTGCTGACGCGCTGGGCGCGCGGCTCTGGCACCCACGAGCTAGCGC 900
Db CTGTTCTCTGTGCTGACGCGCTGGGCGCGCGGCTCTGGCACCCACGAGCTAGCGC 900
Qy GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTACAGCAACTCGCGCTGAACCCG 960
Db GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTACAGCAACTCGCGCTGAACCCG 960
Qy CTGCTACGCGCTTCTGGGCTCGGACTTCGACAGGCTTCGCGCGGTCTGCCCTGCG 1020
Db CTGCTACGCGCTTCTGGGCTCGGACTTCGACAGGCTTCGCGCGGTCTGCCCTGCG 1020
Qy CG 1080
Db CG 1080
Qy CGGAGCTGCAACCGCTTGGGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db CGGAGCTGCAACCGCTTGGGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy AGTGGGCTGGCGCGCGCGCGCGCGCTCTGGGGAGGACCAAGCCCTCTCTGA 1197
Db AGTGGGCTGGCGCGCGCGCGCGCTCTGGGGAGGACCAAGCCCTCTCTGA 1197

RESULT 2
US-09-830-428A-2
; Sequence 2, Application US/09830428A
; Patent No. 6699965
; GENERAL INFORMATION:

; APPLICANT: Takuya WATANABE
; APPLICANT: Yasuko TERAO
; APPLICANT: Yasuhiro SHINTANI
; APPLICANT: Tetsuya OHTAKI
; APPLICANT: Kimiko KANERASHI
; APPLICANT: Chieko KITADA
; TITLE OF INVENTION: No. 6699965el G Protein Coupled Receptor Protein, DNA and its Lig
; FILE REFERENCE: 2001-0272A/WMC/01801
; CURRENT APPLICATION NUMBER: US/09/830,428A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 10-305949
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: JP 11-027710
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: JP 11-057207
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: JP 11-276225
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Rat
; US-09-830-428A-2

Query Match 69.9%; Score 836.4; DB 3; Length 1191;
Best Local Similarity 82.6%; Pred. No. 1.9e-123;
Matches 957; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 1 ATGCACACCGTGGCTACGTCCGGACCCAAACGCGTCTGGGGGGCACCGGCCAAACGCTCC 60
Db 1 ATGCCCGCAGAGCGGACGTTGGGTCCGAAGTGAAGTGGTGGGTCCGCTCAAGGCTTCG 60
Qy 61 GGCTGCCCGGGCTGTGGCGCCAAACGCTTCGGACGGCCAGTCCCTTCGCGCGGGCGGTG 120
Db 61 GGATGCCCGGGCTGCGGTGTCAATGCTCGGATGGCCAGGCTCCGCGCAAGGCCCTCG 120
Qy 121 GACGCTTGGCTCGTGGCGGCTCTTCTTCGCGCGCTGTATGCTTGGGCTGGTGGGGAAC 180
Db 121 GATGCTTGGCTGGTGGCGGCTTCTTCGCTGCCCTATATGTTGCTGGGGTAGTGGGNAAC 180
Qy 181 TCGCTGTCTATCTACGTCATCTGCCGCCACAAGCCGATGCGGACCGTGACCAATCTTAC 240
Db 181 TCACTGTCTATCTTCGTTATCTGCCGCCACAAGCACATGACAGACCGTCAACCAATTTCTAC 240
Qy 241 ATGCCCAACCTGGCGGCCACGAGCTGACCTTCTCTCTGCTGCTGGTCCCTTCACGCC 300
Db 241 ATCGCTAACCTGGCGGCCACAGATGTCACTTCTCTGCTGCTGCTACCCCTTCACGCG 300
Qy 301 CTGCTGTACCGCTGCGCGCTGGGTGCTGGGCGACTTCATGTGCAAGTTCGTAACATAC 360
Db 301 CTCCTCTATCGCTGCCCAACCTGGGTGCTGGGAGACTTCATGTGCAAAATTCGTAACATAC 360
Qy 361 ATCCAGCAGGTCTCGGTGCAAGCCACATGTCGCACTTTGACAGCATGAGTGTGAGCCGC 420
Db 361 ATCCAGCAGGTCTCGGTGCAAGCCACATGTCGCACTTTGACAGCATGAGTGTGAGCCGC 420
Qy 421 TGTACGTGAGGTGTTCCGTTGGCGGCTTGCACCGCCGACCGCCCGCTGGCGGTG 480
Db 421 TGTACGTGAGGTGTTCCGTTGGCGGCTTGCACCGCCGACCTTCACCGCCGACCTCGCGCGCTG 480
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGGCGGGTGTCTGGCGGGTGTCTGCCCTG 540
Db 481 ACTGTGAGCTTAGCATCTGGGTGGGTTCGAGCTGTTCGCGCCCGGTGCTGGCTCTG 540
Qy 541 CACCGCTGTCAACCGGCGCGCGCTTACTGCAAGTGAAGCTTTCGCGAGCGCGCGCTG 600
Db 541 CACCGCTGTGCGCGCGCGCTTCAACCTACTGCAAGTGAAGCTTTCGCGAGCGCGCGCTG 600
Qy 601 GAGCGGCTTCCGACTGTACACCTGCTGGCGGTGCTGGCGGGTGTCTGGCGGGTGTCTGCCCTG 660
Db 601 GAGCGGCTTTCGCGGCTCTCAACCTGCTGGCGCTTATACCTGCTGGCGCTGCTGCCACC 660

Qy	1021	GCGCGGCGCGCCCCCGCGCGCCGCCGGACCCCTGTGGACCCTCGAGGCCCAAC	1080
Db	942	CTGTGGGCGTGCCCCCAGGCGAGCCTCGGCCTGTGTGCGTGCCTGCCG-CGCGGGCAC	1000
Qy	1081	GCGGAGTCAGACCGCTTGGGGTCCACCCGGCCCCCGCAGGGCGCAGACCGAGGAGC	1140
Db	1001	CCACGTGGCAGCGTTGTGGAGCCGAGTCCAGCGACTGTGTGCATCATGACGAGCGCGC	1060
Qy	1141	AGTGGGTGCGCGCGCGGGCTGTGCTCC	1171
Db	1061	GGGGGCCCTTCGTCCCTCGCCCGCGCGCTTC	1091

RESULT 4

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US-08-899-112B-27
; Sequence 27, Application US/08899112B
; Patent No. 6586191
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Linemeyer, David
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Brancheck, Theresa
; APPLICANT: Forray, Carlos
; APPLICANT: Weinshank, Rcihard L.
; APPLICANT: Forray, Carlos
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR2 RECEPTORS AND USES THEREOF
; FILE REFERENCE: 1795/50233-E/JPW/ADM/PL
; CURRENT APPLICATION NUMBER: US/08/899,112B
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/US97/01301
; PRIOR FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: homo sapiens
US-08-899-112B-27

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Query Match	15.6%	Score 186.8	DB 3	Length 1365
Best Local Similarity	51.2%	Pred. No. 3.4e-21		
Matches 601	Conservative 0	Mismatches 522	Indels 51	Gaps 5
QY	3	GCACACGTGGCTACGTCCGACGCCAACACGGTCTCTGGGGGGGACCGGC-----CAACGCC	57	
Db	51	GGAGACCCACACGGCTCAGAGCCCGGGCAGCCTCGGGGTACGGCGACCATGAAGCTC	110	
QY	58	TCGGGCTGCGCCGGGCTGTGGCGCCCAACGCCCTTCGGACGGCGCCAGTCCCTTCGCGCGGGGCC	117	
Db	111	TCGGGCTGCCAG--GGCGCGGAACGCAGCCAGCGCGGGCGCGGGGAGGCTGGCAC	167	
QY	118	GTGAGCGCTGGCTGTGTCGGCTCTTCTTCGCGCGCTGTATGTCTGTGGGCTGTGTGGG	177	
Db	168	CCGAGCGGCTCATCTGTGCGCCCTGCTCTTCGCGCTCATCTTCCTGTGTGGGACCGCTGGC	227	
QY	178	AATCTGCTGTCTATCTACGTCATCTGCGCGGCACAAAGCCGATGCGGACCGTGACCACTTC	237	
Db	228	AACACGCTGTGTGTGGCGGTGCTGCTGCGCGGGCGGCGAGCGGTACAGACTACCAACTG	287	
QY	238	TACATGCCAACCTTGGCGGGCAGCGAGCTTGACCTTTCCTCTGTGCTCGCTCCCTTCACG	297	
Db	288	TTCATCTTAACTTGGCGGTGGCCGACCTGTGTTTTCATCTGTGCTGCGTCCCTTCAG	347	
QY	298	GCCTGTGTACCCGCTGCCCGCTGGGTGCTGGGCGACTTCATGTGCAAGTTCGTCAAC	357	
Db	348	GCCACCATCTACACCTCTGAGCGGTGGGTGTTCGGCTTCGCTGCTGTGTGCAAGGGGGTGCAC	407	
QY	358	TACATCCAGAGGTCTCGGTGCAAGGCCACGTTGTGCCACTCTGACCGCCCATGAGTGTGGAC	417	
Db	408	TTCTCTATCTTCTTACATGACGCCGACGACTTCACGCTGGCGCCGCTCTCCCTGGAC	467	
QY	418	CGTGTGTACGTGAGGTGTTCCGCTTGTGGGGCCCTGTGACCGCGCGCACGCCCGCTGGCG	477	

Db	468	AGGTA	TCTG	GC	CA	TCCG	CTAC	CG	CTAC	CG	CG	AG	TG	CG	CA	CG	CTCG	AA	CG	CG	527	
Qy	478	CTGG	CTGT	CAG	CTC	A	GC	AT	TG	GG	T	AG	GT	CT	CG	CG	CG	GT	CT	CG	CG	537
Db	528	CTGG	CAC	CA	T	CGG	GT	C	A	T	CTG	GG	G	CT	T	CT	CT	CG	GG	CC	CT	587
Qy	538	CTG	C	AC	CG	CT	G	T	C	A	CC	CG	GG	C	G	C	T	A	T	G	C	597
Db	588	T	A	C	T	A	C	G	C	C	A	G	T	G	G	C	A	A	C	T	G	647
Qy	598	CTG	G	A	G	G	G	G	C	T	T	C	G	A	C	T	G	T	G	G	C	657
Db	648	C	G	C	G	C	G	C	C	A	T	G	C	A	C	T	T	T	C	A	G	707
Qy	658	A	C	T	G	C	G	C	T	G	T	A	T	G	G	C	A	T	G	C	A	717
Db	708	CT	G	G	C	T	G	A	C	T	T	G	G	C	T	A	C	T	T	G	G	756
Qy	718	C	C	G	C	C	A	T	A	G	C	C	T	G	C	A	G	A	G	C	G	777
Db	757	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	791	
Qy	778	A	A	G	G	T	C	T	G	G	G	C	G	T	G	T	C	T	T	G	C	837
Db	792	AA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	845	
Qy	838	C	A	G	C	T	G	T	T	C	T	G	T	G	G	C	T	G	G	C	C	897
Db	846	T	G	A	T	G	C	C	C	C	A	C	G	C	T	C	A	T	T	C	G	905
Qy	898	G	C	G	C	T	A	C	G	C	T	T	A	A	G	C	T	G	G	G	T	957
Db	906	G	C	A	C	T	T	A	G	G	T	T	C	G	C	A	T	T	C	T	C	965
Qy	958	C	G	C	T	G	T	C	T	A	G	C	T	T	C	T	G	G	G	C	T	1017
Db	966	C	C	A	T	G	T	T	A	C	G	T	G	T	C	T	C	A	A	G	C	1025
Qy	1018	T	G	C	G	C	G	C	G	C	C	C	C	C	C	C	C	C	C	C	C	1077
Db	1026	G	G	C	T	G	T	G	G	C	G	T	G	C	C	A	G	C	C	T	G	1084
Qy	1078	C	A	C	G	G	A	G	T	G	C	A	C	C	G	C	T	T	G	G	G	1137
Db	1085	C	A	C	C	A	G	T	G	G	A	G	C	T	T	G	A	G	C	C	A	1144
Qy	1138	A	G	A	G	T	G	G	C	G	C	G	G	G	C	T	G	T	G	C	T	1171
Db	1145	G	G	G	G	G	C	C	T	T	G	T	T	C	C	T	T	G	C	C	C	1178

RESULT 5

```

RESOL 5
US-09-011-553-4
; Sequence 4, Application US/09011553A
; Patent No. 6790656
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Linemeyer, David
; APPLICANT: Brancheck, Theresa
; APPLICANT: Forray, Carlos
; TITLE OF INVENTION: DNA Encoding Galanin GALR2 Receptors And Uses Thereof
; FILE REFERENCE: 50233-D-PCT-US/JPW
; CURRENT APPLICATION NUMBER: US/09/011.553A
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: PCT/US97/01301
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/721,837
; EARLIER FILING DATE: 1996-09-27
; EARLIER APPLICATION NUMBER: 08/626,046
; EARLIER FILING DATE: 1996-04-01
; EARLIER APPLICATION NUMBER: 08/626,685

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; EARLIER FILING DATE: 1996-04-01
; EARLIER APPLICATION NUMBER: 08/590,494
; EARLIER FILING DATE: 1996-01-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)..(1265)
US-09-011-553-4

Query Match      15.6%; Score 186.8; DB 3; Length 1365;
Best Local Similarity 51.2%; Pred. No. 3.4e-21;
Matches 601; Conservative 0; Mismatches 522; Indels 51; Gaps 5;

QY 3 GCACACCGTGGTACGTCCGGACCCCAACCGCTCCCTGGGGGGACCGGC-----CAACGCC 57
DB 51 GGAGACCCAGACGGCTGACAGGAGCCGGGACGCTTCGGGGTCAAGCGGCACCATGAACGTC 110
QY 58 TCCGGCTGCCGGGCTGTGGCGCCACACGCTCGGACGGCCCAAGTCCCTTCGCGCGGGGCC 117
DB 111 TCGGGCTGCCAG--GGCCGGGAACGACGACCGAGCGGGCGGGGGAGGCTGGCAC 167
QY 118 GTGGACGCTGGCTGTGCTGCTCTTTCTTCTGGGGGCTGATGCTGCTGGGCTGTGGGG 177
DB 168 CCGAGGGGCTGATCGTGGCCCTCTCTTCTGCGGCTCATCTCTGCGGACCGCTGGGC 227
QY 178 AACTGCTGCTATCTACTGCTATCTGCGGCCACAGCCGATGGGACCTGTGACCACTTC 237
DB 228 AACACGCTGGTGTGGCGGTGTGCTGCGCGGCGGCGGAGCGGTACGACTACCAACCTG 287
QY 238 TACATCGCCAACTGGCGGCCACGAGCGTGAACCTTCTCTGTGCTGCTGCTCCCTTCCAG 297
DB 288 TTCACTCTTAACCTGGGCTGGCGGACCTGTGTTTCACTCTGTGCTGCTGCTTCCAG 347
QY 298 GCGCTGCTGACCGCTGCGGCTGCGGCTGCTGGGCGACTTATGTCGAAGTTCGTCAC 357
DB 348 GCCACCATCTACACCTGACCGCTGGGTGTTGCGGCTGCTGCTGTGCAAGCGGTGCAC 407
QY 358 TACATCCACAGGTCTCGGTGACGAGCCACGTGTGCCACTCTGACCGCCATGAGTGGAC 417
DB 408 TTCTCTCATCTTCTCAACATGACGACGACGAGTTCACGCTGGCGCCGCTCTCCCTGGAC 467
QY 418 CGTGTGTGACGCTGTTCCGTTTGGCGGCTGACCGCGGCGGCGGCGGCTGGCG 477
DB 468 AGGTATCTGGCCATCCGCTACCGCTGCACTCCGCGAGCTGGGACAGCTTGAAACGCG 527
QY 478 CTGGCTGTGACGCTCAGCATCTGGGTAAGCTCTGCGCGGCTGTCTGCGCGGCTGCTCGCC 537
DB 528 CTGGCAGCCATCGGGCTCATCTGGGGGCTGTGCTGCTCTTCTCGGGGCCCTACCTGAGC 587
QY 538 CTGACCGGCTGTACCGGGCGCGCGGCTCTGAGTGAAGGCTTCCCGAGCGCGCGCC 597
DB 588 TACTACCGGAGTGCAGCTGGGCAACCTGACCGGTGTGCCATCCCGCGTGGAGCGCCCT 647
QY 598 CTGGAGCGGCTTCCGCTGTACACCTGTACACCTGTGCGGCTGTACTGCTGCGGCTGCTCGCC 657
DB 648 CCGCGCGGCGCATGAGACTGTGACCTTCTGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 707
QY 658 ACCTGCGCTGTATGCGGCGCATGTCTGCGCACCTGGGCGGGGTGCGCGGCGCGCGCGG 717
DB 708 CTGGGCTGACCTACGCGGCGACCTTTCGCTACCTCTGGGCGCGCTGCG-----756
QY 718 CCGCGCGATAGCGCCCTGACGAGGCGAGGTGTGGCAGAGCGCGCAGCGCGCTGGCGGCC 777
DB 757 -----ACCGGTTGGCGCGGCGGCTGCGGCTGCGGCGCGCGCGCG 791
QY 778 AAGGTCTCGGCTGTGGGCGGCTGTGCTGCTTCTGCGGCTGCTGGGCGCGCGCGCG 837
DB 792 AA-----GCGCAAGGTGACACGATGATCTCTATCTGCGCGCGCTCTTCTGCGCTCTGC 845

RESULT 6
US-08-993-088A-6
; Sequence 6, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fast-Seq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-993-088A-6

Query Match      15.6%; Score 186.2; DB 3; Length 1164;
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QY 421 TGGTACGTGACGGTGTTCCTGGCGCGCTGACCGCGACGCCCGCTGSGCGTG 480
Db 370 TATCTGGGCATCCGCTACCGCTGCACTCCCGAGAGTGGCGACGCCCTGAAACCGCTG 429
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTGTGGCGGGTGTCTGGCGCGGTGTCTGCCCTG 540
Db 430 GCAGCCATCGGCTCATCTGGGGGTGTGGCTGTCTTCTCGGGCCCTACCTGAGCTAC 489
QY 541 CACCGCTGTACCGGGCGCGCTACTGCACTGAGGCTTCCCGAGCGCGCCCTG 600
Db 490 TACCGCCAGTGCAGCTGGCCAACTGACCGTGTGCCATCCCGCGTGGAGCGCCCTGCG 549
QY 601 GAGCGCGCTTCCGCTGTACAACTGCTGGGGCTGTACTCTGCTCGCTGCTGCCAC 660
Db 550 CCGCGGCATGCACTGTGCACTTGTCTTACGCTACTCTCTCTGCTGTGCTGTTCTC 609
QY 661 TCGCGCTGTATCGGCGCATGTGCGGCACCTGGCGCGGTGCGCGTGGCGCGCGCC 720
Db 610 GGCCTGACCTACGCGGACCTTGGCTACCTCTGGCGCGCTG----- 655
QY 721 GCCGATAGCGCCTGAGGGGAGGTGTGGCGAGCGGCGAGCGCGTGGCGGCCAAG 780
Db 656 -----ACCGGTGGCGCGGGCTCGGGTGGCGCGCGCCAA- 692
QY 781 GTCTCGCGCTGTGGCGCGCTGTCTGCTCTTGGCGCGCTGTGGCGCGCCATCCAG 840
Db 693 -----GCGCAAGTGACACGATATCTCTCATCTGTGGCGCGCTCTTCTGCGCTGTG 747
QY 841 CTGTTCTGTGCTGACGCGCTGGCGCGCGCGGCTCTGGCACCCACGACGCTACGCC 900
Db 748 ATGCCCCACACCGCTCATCTCTGCTGTGTGGCGAGTTCGCGCTACGCGCGCC 807
QY 901 GCCTACGCGCTTAAAGCTTGGCTCACTGCACTGTCTACAGAACTCCGCGCTGAACCG 960
Db 808 ACTTATGGCTTGGATCTCTCGACCTGTCTCTAGCGCAACTCTCTGCGTCAACCCC 867
QY 961 CTGCTTACGCTTCTTGGCTGCACTTCCGACAGGCTTCCGCGCGCTTGGCGCGCTG 1020
Db 868 ATCGTTACGCGCTGTCTTCAAGCACTTCCGCAAGGCTTCCGACGATCTGCGCGGCG 927
QY 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 928 CTGCTTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 986
QY 1081 GCGGAGCTGCACCGCTTGGGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 987 CCACAGTGGCAGCGTGTGGAGCGGAGTCCAGCGACCTTTTGCACTGAGCGGCGCG 1046
QY 1141 AGTGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1171
Db 1047 GCGGCGCGCTTCTGCTTCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077
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RESULT 8

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US-09-603-680-6
; Sequence 6, Application US/09603680
; Patent No. 6544753
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; TITLE OF INVENTION: GALANIN RECEPTOR GALT2 AND
; NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/603,680
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; APPLICATION NUMBER: 08/993,088
; FILING DATE: 18-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846 CA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-603-680-6
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Query Match 15.6%; Score 186.2; DB 3; Length 1164;
Best Local Similarity 51.4%; Pred. No. 4.3e-21;
Matches 540; Conservative 0; Mismatches 466; Indels 43; Gaps 3;

QY 121 GACGCTGGCTGTCGCGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGGCTGTGGGGAAAC 180
Db 70 GAGGCGGTGTCGCGCGCTCTTCTTCGCGCTGATGCTTCTTCGCGCGACCGTGGGCAAC 129
QY 181 TCGCTGTGTCATGTCATCTGCGCGCAAGCGGATGCGGACCGTGACCACTTCTAC 240
Db 130 ACCTGTGTGTCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 189
QY 241 ATGCGCAACCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 190 ATCTTAACTGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 249
QY 301 CTGCTGTACCGCTGCGCGCGCTGGGTGTGGCGCGCTTCTCATGTGCAAGTTCGTCAACTAC 360
Db 250 ACCATCTACACCTGGACCGCTGGGTGTTCGCGCTGCTGCTGCAAGCGGTGCACTTC 309
QY 361 ATCCAGCAGGTCTGGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 310 CTCATCTTCTCACCATGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 369
QY 421 TGGTACGTGACGGTGTTCCTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 370 TATCTGGGCATCCGCTACCGCTGCACTCCCGAGAGTGGCGACGCCCTGAAACCGCTG 429
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTGTGGCGGGTGTCTGCGCGCGGTGTCTGCCCTG 540
Db 430 GCAGCCATCGGCTCATCTGGGGGTGTGGCTGTCTTCTTCGCGCGCGCTACCTGAGCTAC 489
QY 541 CACCGCTGTACCGGGCGCGCGCGCTACTGCACTGAGGCGCTTCCCGAGCGCGCGCGCTG 600
Db 490 TACCGCCAGTGCAGCTGGCCAACTGACCGTGTGCCATCCCGCGTGGAGCGCGCGCTGCG 549
QY 601 GAGCGCGCTTCCGCTGTACAACTGCTGGGGCTGTACTCTGCTGCGCGCTGTGCCAC 660
Db 550 CCGCGGCATGCACTGTGCACTTGTCTTACGCTACTCTGCTTCTGCTGTGCTGTTCTC 609
QY 661 TCGCGCTGTATGCGCGCATGTGCGGCACCTGGCGCGGTGCGCGCTGGCGCGCGCGCG 720
Db 610 GGCCTGACCTACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
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Qy 721 GCCGATAGCGCCTGTCAGGGCAGGTGCTGCGAGAGCGCGAGGCGCGCTGCGGGCCCAAG 780
Db 656 -----ACCGGTGGCGGCGCTGGGTGTCGGGCGGCCAA - 692
Qy 781 GTCTCGGGCTGGTGGCGCGTGGTCTGTCTTTCGCGCGCTGCTGGGGCCCAATCCAG 840
Db 693 -----GCGCAAGGTGACAGCATGATCTCATCGTGGCGCGGCTCTTCTGCGCTCTGTGG 747
Qy 841 CTGTTCTGTGTGCTGACGGCGCTGGGCGCGCGGCTCTTGGCACCCAGCAGCTAGCGC 900
Db 748 ATGCCCAACACGGGCTCATCTCTGCTGTGGTTCGGCGAGTTCGCGCTCACGCGGCC 807
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Qy 961 CTGCTCTAGCGCTTCTGGGCTCGCACTTCGACAGGCGCTTCGGCGGGTCTGCGCCCTG 1020
Db 868 ATCGTTTACGGCGTGGTCTCCAAGCACTTCGCGCAAGGCTTCGACGATCTGGCGGGC 927
Qy 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 928 CTGCTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 986
Qy 1081 GCGGAGCTGACCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 987 CCACAGTGGCAGCGTGTGGAGCGGAGTCCAGCGACCTGTTGCACATGACGAGGCGCG 1046
Qy 1141 AGTGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1171
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RESULT 9

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US-09-826-509-504
; Sequence 504, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: NO. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR APPLICATION NUMBER: 2001-04-05
; PRIOR FILING DATE: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 504
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-504
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Query Match 15.4%; Score 184.6; DB 3; Length 1164;

Best Local Similarity 51.3%; Pred. No. 7.6e-21;

Matches 539; Conservative 0; Mismatches 469; Indels 43; Gaps 3;

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Qy 121 GACCGCTGGCTGCGCGCGCTCTTTCGCGCGGCTGATGCTGCGGCGCTGGTGGGGAAC 180
Db 70 GAGCGGTGTCATGCGCGCGCTCTTTCGCGCGGCTGATGCTGCGGCGCTGGGGAAC 129
Qy 181 TCGGTGTGTCATGCTGATCTGCGCGCACCAAGCGATGCGGACCGGTGACCAACTTCTAC 240
Db 130 ACGTGTGTGCTGGCGGTGCTGCTGGCGCGCGGCGGCTGACCAACTTCTGTC 189
Qy 241 ATCGCCAACTGGCGGCGCACGAGCTGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 190 ATCCTTAACCTGGCGGTGGCGGACCTGTGTTTCTATCTCTGCTGCTGCTGCTGCTGCT 249
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Qy 301 CTGCTGTACCGGCTGCCGCGTGGGTGCTGGGCGACTTTCATGTGCAAGTTCGTCAACTAC 360
Db 250 ACCATCTACACCTTGGAGCGGTGGGTGTTTGGGCTGCTGCTGTGCAAGCGGTGCATTC 309
Qy 361 ATCCAGCAGGTCTCGGTGCAAGCCACGTGTGCCACTCTGACCCGCAATGAGTGTGAGCCG 420
Db 310 CTATCTTCTCACAATGACCGCAGCAGCTTTCACGCTGGCGCGGCTCTCCCTGAGACAG 369
Qy 421 TGGTACGTGAGGTGTTCCGTTGGCGCGGCTGACCGCGCAGCGCCCGCTGGCGCTG 480
Db 370 TATCTGCCATTCGCTACCCGCTGCACTCCGCGAGCTGCGCAGCTCGAAGACGCGCTG 429
Qy 481 GCTGTAGCCTCAGCATCTGGGTAGGCTCTGCGCGGCTGTCTGCGCGGCTGCTGCCCTG 540
Db 430 GCAGCCATCGGCTCATCTGGGGGCTGCTGCTGCTTCTCCGGGCGCTACCTGAGCTAC 489
Qy 541 CACCGCTGTACCCGGCGCGCGGCTAATGCAAGTGAAGGCTTCCGACGCGCGCGCTG 600
Db 490 TACCGCGAGTCCGAGCTGGCGCAACTGACGCTGTGCCATCCCGGTGGAGCGCGCTCGC 549
Qy 601 GAGCGCGCTTGCACATGTGCTACACCTGCTGGCGCTGTACCTGCTGCGGCTGCTGCCAC 660
Db 550 GCGCGCGCTTGCACATGTGCTACACCTGCTGGCGCTGTACCTGCTGCTGCTGCTGCTG 609
Qy 661 TGCGCTGTATGCGGCGCATGTGCGCGCATCTGGGCGCGGCTGCGCGCTGCGCGCGCG 720
Db 610 GCGCTGACCTACGCGCGCATCTGCGGCTAATCTGCGGCTGCTGCGCGCGCGCTG 655
Qy 721 GCGGATAGCGCTTGCAGGGGCGAGGTGCTGGCAGAGCGCGCAGCGCGCTGCGGCGCAAG 780
Db 656 -----ACCGGTGGCGCGGCTGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 692
Qy 781 GTCTCGCGGCTGGTGGCGCGGCTGCTGCTGCTGCGCGGCTGCTGGGCGCGCGCGCGCG 840
Db 693 -----GCGCAAGGTGAAACGCATGATCTCATCTGCGCGGCTCTTCTGCTCTGCTGG 747
Qy 841 CTGTTCTGTGTGCTGACGGCGCTGGGCGCGCGGCTCTTGGCACCCAGCAGCTAGCGC 900
Db 748 ATGCCCAACACGGGCTCATCTCTGCTGTGGTTCGGCGCGCTTCCGCTCACGCGCGCG 807
Qy 901 GCCTACGCGCTTAAGACCTGGGCTCACTGATGCTTCTACAGCAACTCGCGCTGAACCCG 960
Db 808 ACTTATGGCTTCGATCTCTGCACTGCTGCGCGCTGCTTCTTACGCAACTCTCTGCGTCA 867
Qy 961 CTGCTCTAGCGCTTCTGGGCTCGCACTTCGACAGGCGCTTCGCGGGTCTGCGCCCTG 1020
Db 868 ATCGTTTACGGCGTGGTCTCCAAGCACTTCGCGCAAGGCTTCGACGATCTGGCGGGC 927
Qy 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 928 CTGCTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 986
Qy 1081 GCGGAGCTGACCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 987 CCACAGTGGCAGCGTGTGGAGCGGAGTCCAGCGACCTGTTGCACATGACGAGGCGCG 1046
Qy 1141 AGTGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1171
Db 1047 GGGGGCGCGTTCGCTCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1077
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RESULT 10

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US-07-816-283-9
; Sequence 9, Application US/07816283
; Patent No. 5436155
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
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NAME/KEY: CDS
LOCATION: 28...1281
US-08-417-103-9

Query Match 14.6%; Score 175; DB 2; Length 1296;
Best Local Similarity 53.8%; Pred. No. 2.5e-19;
Matches 520; Conservative 0; Mismatches 405; Indels 42; Gaps 6;

79 GCCAACGCTCGGACGGCCCACTCCCTTCGCGCGGGCGGTGGACGCTGCTGCTGTCGCG 138
112 GCGAACGCTGTCGGCGGGCCCAAGCCCGGACGGCTGGCGGTCTGATGCTGATCCCC 171
139 CTCTTCTTCGCGCGCTGATGCTGCTGGGCTGCTGGGAACTCGCTGGTCACTACGTC 198
172 CTGGTCTACCTGGTGTGGTGGGCTGCTGGGTAACCTGCTGCTCATCTATGTG 231
199 ATCTGCGCCACAGCGATCGGACCGTGTACCACTCTTACATCGCCCACTGGCGCC 258
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259 ACGGACGCTGACCTTCCTCTGCTGCTGCCCTTCACGGCCCTGCTGTACCCGCTGCC 318
292 GCCGACGAGCTCTTCATGCTG---GGGCTGCCCTTCCTGGCGGCCGAGACGCTGTCC 348
319 GGTGGGTGCTGGGCGACTTCATGTGCAAGTTCTGTCACACTACATCCACAGGTTCTGGTG 378
349 TACTGGCCCTTCGGCTCCCTCATGTGCGCCCTGCTGATGGGGTGGATGGCATCAACCA 408
379 CAGGCCAGCTGTCACACTCTGACGCCATGAGTGTGGACGCTGTTAGTACGAGTGTTC 438
409 TTCACGAGCATATTTGCTGCTGACTGTATGAGCGTGGACCGCTACCTGGCGGTGAT 468
439 CCGTTGCGCGCCCTGACCGCGCACGCGCCGCTGGCGCTGGCTGTGCTGAGCTCAGCATC 498
469 CCCACCGCTGCGCCGCTGGGCGACAGCTCGGTGGCGCCGACGCTCAGCGCGCTGTG 528
499 TGGTAGGCTCTGCGCGCGGTGTGCGCGCGTGTGCGCCCTGCAACCGCTGTCAACCGGG 558
529 TGGGTGGCTCAGCGGTGGTGTGCGCGCTGCTGCTGGGAGTGGTCTTCTGGGAGTGGCC 588
559 CCGCGCGCTACTGACGTAG---GCCTTCCCGACGCGCGCCCTGGAGG---CGCTTTCGA 615
589 ATGACACCTGCCACATGACGTGGCGCGAGCGCGCGCGCTGGCGAGCGCGCTTATC 648
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649 ATCTACAGCGCGGACTGGGCTTCTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
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709 CTCATCGTGTGAGGTGGC-----TCAGTGGGCGCGGGGTGGGCGACCGCTC 758
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759 GTGCCAGCGCGCGCGCGCTCCGAAAC-----GCAGGGTCAACGCGCATGGTG 804
796 GCGGCGGTGCTGCTCTTTCGCGCGCTGCTGGGCGCCCATTCACGTGCTTCTGCTGCTG 855
805 GTGCGCGGTGGGCGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
856 CAGGCGCTGGCGCGCGCGGTCTTGGCACCCACGACGTACGCGCGCTACGCGCTTAAG 915
865 AACGTGGTGGCCACTGCCGAGGAGC-----CTGCGCTTCTTTGGGCTCTAC 912
916 ACCTGGGCTCACTGATGCTCTACAGCACTCGGGCTGAGACCGCTGCTTACGCTTC 975
913 TTCCTGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
976 CTGGGCTGCGACTTCCGACAGCGCTTCCGCGCGGTCTGCCCTTGGCGCGCGCGCGCC 1035
973 CTCCTCTACCGCTTCAAGCAGGGCTTCCGCGAGGGTCTGCTGCGGCGCTCCCGCGGTG 1032
1036 GCGCGCC 1042

Db 1033 CGCAGCC 1039

RESULT 12
US-09-016-434-1321
; Sequence 1321, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1321:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g338498
; US-09-016-434-1321

Query Match 14.6%; Score 175; DB 3; Length 1413;
Best Local Similarity 53.8%; Pred. No. 2.5e-19;
Matches 520; Conservative 0; Mismatches 405; Indels 42; Gaps 6;

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Qy 139 CTCTTCTTCGCGCGCTGATGCTGCTGGGCTGCTGGGAACTCGCTGGTCACTACGTC 198
Db 242 CTGGTCTACCTGGTGTGGTGGGCTGCTGGGTAACCTGCTGCTCATCTATGTG 301
Qy 199 ATCTGCGCCACAGCGATCGGACCGTGTACCACTCTTACATCGCCCACTGGCGCC 258
Db 302 GTCTGCGGCACAGCGCAGCCCTTCAGTCAACACGCTTACATCCCTCAACTGGCGTG 361
Qy 259 ACGGACGCTGACCTTCCTCTGCTGCTGGCTTCCCTTCACGGCGCTGCTGTACCCGCTGCC 318
Db 362 GCCGACGAGCTCTTCATGCTG---GGGCTGCCCTTCTTGGCGGCCGAGACGCTGTGCC 418
Qy 319 GGTGGGTGCTGGGCGAGCTTCATGTGCAGAGTTCTGCTCAACTACATCCAGAGGTCTCGGTG 378

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	Matches 346;	Conservative 0;	Mismatches 233;	Indels 15;	Gaps 2;
Qy	115	GC	GTGACGCCCTGGCTGTCGCGCTCTTCTTCGCGCGCGTGTGTCGTCTGGCGCTGTG	174	
Db	88	GG	GGTGAGAACTTCGTACGCTGGTGGTGTTCGGCCGTATCTTCGCGCTGGCGGTGCTG	147	
Qy	175	GG	GAATCGCTGTGTCATCTATCGTCATCTGCGGCCACAAGCCGAT-----GCGGACCGCTG	228	
Db	148	GG	CAACAGCCTAGTGATCAGCGTCTGGCGCGCAGCAGCGCGGCAAGCCCGGAGCACC	207	
Qy	229	AC	CAACTTCTACATCGCCAACTTGGCGGCCACGACGTCCTTCCTCTGTCTGTGCGTC	288	
Db	208	AC	CAACTGTTCATCTCAACCTTGGCATCGCCGACCTGGCCTACCTGCTCTTCTGCAATC	267	
Qy	289	CC	CTTACGCGCCCTGTGTATCCCGCTGCCCGGTGGGTGCTGGCGCACTTCATGTGCAAG	348	

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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4: gb_hc:*
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9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*
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SUMMARIES

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3	627.6	52.4	1032	AL568705	AL568705
4	593.4	49.6	872	AL541044	AL541044
5	359.8	30.1	503	BF470621	UI-M-BH3-
6	347.6	29.0	600	CK623581	milli03.y
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8	277.6	23.2	759	DN693330	AGENCOURT
9	275.8	23.0	591	CO039966	UI-M-BH3-
10	246.2	20.6	465	CN367647	170005321
11	244	20.4	507	CR982913	CR982913
12	240.2	20.1	887	BM944117	UI-M-EHOp
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15	195.8	16.4	960	CA487873	AGENCOURT
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18	173.4	14.5	1257	AY400332	Homo sapi
19	173.2	14.5	454	AI823800	wj14h01.x
20	169.8	14.2	721	CF147813	AGENCOURT
21	166.4	13.9	1287	AY400334	Mus muscu
22	161	13.5	815	BZ197821	CH230-416

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c 25	156.2	13.0	460	1	AI819198	AI819198 wj32F02.x
c 26	155	12.9	730	6	CF147825	CF147825 AGENCOURT
c 27	154.2	12.9	441	5	BY260374	BY260374 BY260374
28	152	12.7	853	10	AY409236	AY409236 Homo sapi
29	149.6	12.5	798	5	BX078215	BX078215 BX078215
30	146.6	12.2	1257	10	AY400333	AY400333 Pan trogl
31	142.6	11.9	241	7	CO881664	CO881664 BovGen.09
32	138.6	11.6	668	7	CO918721	CO918721 AGENCOURT
33	136	11.4	136	11	DQ046674	DQ046674 Homo sapi
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35	134.8	11.3	1918	4	AK053776	AK053776 Mus muscu
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38	129	10.8	468	5	BX281894	BX281894 BX281894
39	128.6	10.7	849	10	AY409237	AY409237 Pan trogl
40	122.2	10.2	937	11	CNS03GSG	AY4243385 Tetraodon
41	121	10.1	1113	10	AY420480	AY420480 Homo sapi
42	120.4	10.1	1119	11	DQ035375	DQ035375 Homo sapi
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45	111.8	9.3	899	7	CN838037	CN838037 AGENCOURT

ALIGNMENTS

RESULT 1
CR621438
LOCUS full-length cDNA clone CS0DE005YC17 of Placenta of Homo sapiens
DEFINITION (human)
ACCESSION CR621438.1 GI:50502245
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope.
REFERENCE 2 (bases 1 to 1582)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. 1582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005YC17"
/tissue type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 99.9%; Score 1195.4; DB 4; Length 1582;
Best Local Similarity 99.9%; Pred. No. 1.1e-206;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCACACCGCTGCTACGTCGGGACCCACACGCTCCTCGGGGGACACGGCCCAACGCCTCC 60
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161 ATGCACACCGCTGCTACGTCGGGACCCACACGCTCCTCGGGGGACACGGCCCAACGCCTCC 220
Qy 61 GCTCTCCCGGGGTGTGGGCGCAACCGCTTCGACAGCGCCAGTCCCTTCGCCCGGGCGCGGTG 120
Db |||||
221 GCTCTCCCGGGGTGTGGGCGCAACCGCTTCGACAGCGCCAGTCCCTTCGCCCGGGCGGTG 280
Qy 121 GACGCTCGCTGCTGCCGCTCTCTTCGCGGGCGCTGATGCTGCTGGGCTCTGGTGGGGAAC 180
Db |||||
281 GACGCTCGCTGCTGCCGCTCTCTTCGCGGGCGCTGATGCTGCTGGGCTCTGGTGGGGAAC 340
Qy 181 TCGCTGCTCAGTACGTCATCTGCCGCGCACAGCGGATGCGGACCGTGCACCACTTCTAC 240
Db |||||
341 TCGCTGCTCAGTACGTCATCTGCCGCGCACAGCGGATGCGGACCGTGCACCACTTCTAC 400
Qy 241 ATCGCCAACTGGCGGCCACGACGATGACCTTCCTCTGCTGCTGCTGCCCTTCACGGCC 300
Db |||||
401 ATCGCCAACTGGCGGCCACGACGATGACCTTCCTCTGCTGCTGCTGCCCTTCACGGCC 460
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Db |||||
461 CTGCTGTACCGCTGCTGCCGCTGGGTGTGGGCGACTTCATGTGCAAGTTCTCAACTAC 520
Qy 361 ATCCAGCAGGCTCGGTGCGGCCACGCTGTCCTCTGCTGCTGCTGCCCTTCACGGCC 420
Db |||||
521 ATCCAGCAGGCTCGGTGCGGCCACGCTGTCCTCTGCTGCTGCTGCCCTTCACGGCC 580
Qy 421 TGGTACGTGAGGCTGCTCCGCTTGGCGGCTGTCACCGCCGCTGCTGCCCTTCACGGCC 480
Db |||||
581 TGGTACGTGAGGCTGCTCCGCTTGGCGGCTGTCACCGCCGCTGCTGCCCTTCACGGCC 640
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGTGTCTGCGCGGCTGCTGCCCTG 540
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641 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGTGTCTGCGCGGCTGCTGCCCTG 700
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Db |||||
701 CACGCGCTGTCACCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
Qy 601 GAGCGCGCTTTCGCACTGACAACTGCTGCGGCTGTACCTGCTGCTGCTGCTGCTGCTGCTG 660
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761 GAGCGCGCTTTCGCACTGACAACTGCTGCGGCTGTACCTGCTGCTGCTGCTGCTGCTGCTG 820
Qy 661 TCGCGCTGCTATGCGGCCATGCTGCGGCCATGCTGCGGCCATGCTGCGGCCATGCTGCGGCC 720
Db |||||
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Db |||||
881 GCGGATAGCGCCTGACGGGCGAGTGTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 940
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Qy 841 CTGTTCTGCTGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCG 900
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1001 CTGTTCTGCTGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCGGCCGCTGCG 1060
Qy 901 GCCTACGCGCTTAGACCTGGGCTCAGTGCATGCTCTACAGCACTCTCGGCTGACCCG 960
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1061 GCCTACGCGCTTAGACCTGGGCTCAGTGCATGCTCTACAGCACTCTCGGCTGACCCG 1120
Qy 961 CTGCTCTACGCTTCTCTGGGCTCGCATCTTCGACAGGCTTTCGCGCGGCTCTGCCCTGCG 1020
Db |||||
1121 CTGCTCTACGCTTCTCTGGGCTCGCATCTTCGACAGGCTTTCGCGCGGCTCTGCCCTGCG 1180
Qy 1021 GCG 1080
Db |||||
1181 GCG 1240
Qy 1081 GCGGAGCTGCACCGCTCGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1140

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1241 GCGGAGCTGCTCCGCCCTGGGGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1300
Qy 1141 AGTGGCTGGCGCGCGCGCGCGCTGTGGCTCTGGGGGAGGAGCAACCGCCCTCTCTGA 1197
Db |||||
1301 AGTGGCTGGCGCGCGCGCGCGCTGTGGCTCTGGGGGAGGAGCAACCGCCCTCTCTGA 1357

RESULT 2
AK039628
LOCUS
DEFINITION
Mus musculus adult male spinal cord cDNA, RIKEN full-length
enriched library, clone:A330075J02 product:G-PROTEIN-COUPLED
RECEPTOR GPR54 (G PROTEIN-COUPLED RECEPTOR 54), full insert
sequence.
AK039628
VERSION
AK039628.1 GI:26333372
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
(bases 1 to 3075)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
 URL: <http://genome.gsc.riken.jp/>
 URL: <http://fantom.gsc.riken.jp/>

COMMENT

FEATURES

source

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Query Match      69.4%; Score 830.4; DB 4; Length 3075;
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Matches 954; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

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Db      1705  ATGGCCACCGAGCGACATGGCTCCCAATGTGACCTGGTGGGCTCCGTCACACGCTTCA 1764

QY      61  GCCTGCCGGGTGTGGCGCCAAACGCTCGAGCGGCCAGTCCCTTCGCGCGGCCGCTG 120
Db      1765  GGATGCCACGAGGTGGCGGTCAACGCTCGGATGACCCCAAGGCTCTGCGCAAGGCCCTCG 1824

QY      121  GACGCTGGCTGTGCGCGCTCTTCTTTCGGGGCGCTGATGCTGCTGGCGCTGTGGGGAAC 180
Db      1825  GATGCTGTGCTGGTGTCCCTGTTTTCGCTACACTCATGTGCTTGGGCTGTGCGGAAC 1884

QY      181  TCGTGGTCACTACGTCATCTGCGCCCAAGCGCATCGGACCGTGCACCAACTTCTAC 240
Db      1885  TCATTGGTCACTACGTTATCTGCGCCCAAGACCATGCAGACAGTACCAACTTCTAC 1944

QY      241  ATCGCCACCTGGCGCCAGGACGCTGACCTTCCTCTGCTGTGCTGCTCCCTTCAGGCC 300
Db      1945  ATCGTAACTGGCTGCCACAGACGTCATTTCTTCTACTGTGCTGCTGCTTCCCTTCA 2004

QY      301  CTGCTGTACCGCTGCCCGGTGGGTGTGGGCGACTTCATGTGCAAGTTCGTCAACTAC 360
Db      2005  CTCCTTACCGCTGCCCGCTGGGTGTGGGAGACTTCATGTGCAATTCGTCAACTAC 2064

QY      361  ATCCAGCAGGTCTCGGTGACGCCACAGTGTGCCACTCTGACCGCCATGATGTGGACCG 420
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QY      661  TCGCGCTGCTATGCGGCGCATGCTGCGCCACCTGGGCGCGGTGCGCGTGTGCGCGCGCC 720
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QY      721  GCCGATACGCGCTTTCAGGCGCGAGTGTGCGAGAGCGCGAGCGCGCTGCGCGCGCCAG 780
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QY      781  GTCTCGCGCGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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QY      901  GCCTACGCGCTTACAGACCTGCGGCTCACTGCAATGTCTTACAGAACTCCGCGCTGAACCG 960
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QY      1141  AGTGGGCTGGCGCGCGCGG 1160
Db      2845  CTTGTGTGCTGCTGCGCGCTG 2864

RESULT 3
AL568705/c
LOCUS      AL568705 Homo sapiens PLACENTA Homo sapiens cDNA clone CS05005YCL17
DEFINITION      3-PRIME, mRNA sequence.
ACCESSION      AL568705
VERSION        AL568705.3 GI:46235036
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homidae; Homo.
REFERENCE      1 (bases 1 to 1032)
AUTHORS       Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
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	/note="Organ: brain; Vector: pYX-Asc; Site:1: Ecor I; Site:2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCACACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	
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	Query Match 20.1%; Score 240.2; DB 3; Length 887;	
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Qy	1 ATGCACACCGTGGCTACGTCGGACCCCAACCGCTCTCGGGGGGACCGGCCAACGCGCTCC 60	
	Db 412 ATGGCCACCGAGCGACATGGCTCCCAATGTGACCTGGTGGCTCCGTCACACGCTTCA 471	
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Qy	181 TCGCTGGTCATCTACGTCATCTGCGGCCACAGCCGATCGGACCGTGCACCAACTTCTAC 240	
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Qy	241 ATCGCCAACTGGCGGCCACGACGTGACCTTCCTCTGCTGTGCTGCCCTTCACGGCC 300	
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Qy	361 ATCCAGCAGGTCCTCGGTGCAGGC 383	
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RESULT 13	BX514847	
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DEFINITION	BX514847 NCI CGAP Mam5 Mus musculus cDNA clone IMAGEp998N198526 ;	
	IMAGE:3488082, mRNA sequence.	
ACCESSION	BX514847	
	VERSION	
KEYWORDS	BX514847.1 GI:32294125	
	EST.	
SOURCE	Mus musculus (house mouse)	
	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia;	
	Sciurognathi; Muridea; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 487)	
	Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.	
TITLE	Mouse Unigeneset - RZPD2	
	Unpublished (2003)	
JOURNAL	Contact: Ina Rolfs	
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
COMMENT	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany	
	RZPD; IMAGp998N198526.	
	RZPDLIB; I.M.A.G.E. cDNA Clone Collection;	
	Mouse Unigeneset - RZPD2 (RZPDLIB No.981)	
	http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=981	
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	
	Heubnerweg 6, D-14059 Berlin, Germany	
	Tel: +49 30 32639 101	
	Fax: +49 30 32639 111	
	www.rzpd.de	
	This clone is available royalty-free from RZPD;	
	contact RZPD (clone@rzpd.de) for further information. Seq primer:	
FEATURES	SP6, Primer sequence: ATTTAGGTGACACTATAG.	
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ORIGIN	Query Match 19.5%; Score 233.8; DB 5; Length 487;	
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Qy	241 ATCCGCAACTGGCGGCCACGACGTGACCTTCCTCTGCTGCTGGTCCCTTCACGGCC 300	
	Db 387 ATCGCTAACCTGGCTGCCACAGAGCTCACTTCTCTACTGTGCTGGTCCCTTCACCGCA 446	
Qy	301 CTGCTGTACCCGCTGCCGGCTGGGTGTGCGGCGACTTCAT 341	
	Db 447 CTCCTCTACCCGCTGCCGCTGGGTGCTGGAGACTTCAT 487	
RESULT 14	BE309856	
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	671 bp mRNA linear	
	EST 26-OCT-2000	

DEFINITION 601093479F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:348082 5', mRNA sequence.

ACCESSION BE309856

VERSION BE309856.1 GI:9168690

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 671)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Place: LHAM8526 row: n column: 19
High quality sequence stop: 420.

FEATURES

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Location/Qualifiers

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5. /clone="IMAGE:348082"

6. /tissue_type="tumor, gross tissue"

7. /dev_stage="7 months"

8. /lab_host="DH10B"

9. /clone_lib="NCI CGAP Mam5"

10. /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN

Query Match 16.6%; Score 198.6; DB 2; Length 671;

Best Local Similarity 69.2%; Pred. No. 5.3e-26;

Matches 330; Conservative 0; Mismatches 139; Indels 8; Gaps 4;

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QY 61 GGCTGCCCGGGCTGTGGCGCCCAACGCGCTCGAGCGGCCAGTCCCTTCGCGCGGGCGGTG 120

DB 187 GGATGCCACCGGTGCGGTGTCAACGCGCTCGGATGACCCAGGCTCTGCGCCAAAGGCCCTG 246

QY 121 GAGCGCTGCGTGTGCGCGCTCTTTCTTCGCGCGCTGATGCTCTGGCGCTGTGGGGAC 180

DB 247 GATGCTGTGCTGTTCCCTGTTTTCGCTACACTCATGTTGCTGGGCTGTGCGGAAC 306

QY 181 TCGTGGTTCATCTACGTCTATCTCGGCCACAAGCCGATGCGGACCGTGCACCAAC-TTCTA 239

DB 307 TCATTGGTTCATCTACGTTATCTGCGCCACAAGCACATGCAGACGTTACCAACTTCTA 366

QY 240 CATCGCAACCT-GGGGGCAGGAGTGACCTTCCTCTGTGTGCTGCGTCCCTTCACGG 298

DB 367 CATCGTAACCTGGGTGCGCAGACGTCACCTTCTACTGTGCTGCGTCCCTTTACGG 426

QY 299 CCTGTGTACCGCTGCGCGCTGGGTGCTGGGGACTTCATGTGCAAGTTGTCAACT 358

DB 427 AATCCTCTAACCGTCCCGCTGTGTGCTGGGAGACTTCTGTGGCAATTGCTGACT 486

QY 359 ACATCC---AGCAGGTCTCGGTGCGAGGCCACCGTGTG---CCACTCTGACCGCCATGAGTG 412

DB 487 TCATCCCGCCAGGTTCTCCGTTGCAAGCCACATGTGTCCACTCTCTGTACGGGGCTTAGTGT 546

QY 413 TGGACCGCTGTACGTGACGGTGTTCGGTTGCGCGCCCTGCACCGCCGACGCCCC 469

DB 547 TGGCCCGCGGTTGTGACTGTGTTCGCCGGGTGCATTTACCGCGCGTGGCGC 603

RESULT 15

CA487873

LOCUS CA487873

DEFINITION AGENCOURT_10811154 MAPcL Homo sapiens cDNA clone IMAGE:6719495 5', mRNA sequence.

ACCESSION CA487873

VERSION CA487873.1 GI:24948297

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 960)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Place: LHAM14277 row: h column: 23
High quality sequence start: 40
High quality sequence stop: 488.

FEATURES

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Location/Qualifiers

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1. /organism="Homo sapiens"

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4. /clone="IMAGE:6719495"

5. /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCap"

6. /lab_host="EMDH10B"

7. /clone_lib="MAPcL"

8. /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN

Query Match 16.4%; Score 195.8; DB 6; Length 960;

Best Local Similarity 88.7%; Pred. No. 1.7e-25;

Matches 212; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 480 GGCTGTGACGCTCAGCATCTGGGTAGGCTCTGCGCGGTGTCTGCGCGGTCTCGCCCT 539

DB 355 GGTCTTTCATCTGGTGTGGCACAGGCTCTGCGCGGTGTCTGCGCGGTCTCGCCCT 414

QY 540 GCACGCGCTGTACCCGCGCGCGCGCTACTCAGTAGGCGCTTCCCGACGCGCGCT 599

DB 415 GCACGCGCTGTACCCGCGCGCGCGCTACTCAGTAGGCGCTTCCCGACGCGCGCT 474

QY 600 GGAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACCTGTGCGCTGTCTGCCAC 659

DB 475 GGAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACCTGTGATGACGCTGTCTGCCAC 534

QY 660 CTGCGCTGTCTATGCGGCCATGCTGCGCCACCTGCGCGGGTTCGCGCGCGCCCGCGC 718

Db 535 CTGCGCCTGCTATGCGGCCATGCTGCCCCACCTGGGCCGGGTCCGCTCCGCCCCCCCCC 593

Search completed: February 15, 2006, 06:06:48
Job time : 5405 secs

;

;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 01:15:56 ; Search time 810 Seconds
(without alignments)
9848.935 Million cell updates/sec

Title: US-10-771-417-6
Perfect score: 1197
Sequence: 1 atgcacacgtggtacgtc.....aggacaacgccccctctctga 1197

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197	100.0	1197	3	AAA39343
2	1197	100.0	1197	4	ADT07921
3	1197	100.0	1197	8	AB242844
4	1197	100.0	1197	11	ADN39429
5	1197	100.0	1197	11	ADN39504
6	1197	100.0	1197	12	ADL19584
7	1197	100.0	1197	12	ADO29925
8	1197	100.0	1197	14	ACL38952
9	1197	100.0	1197	14	ADZ68968
10	1195.4	99.9	1197	3	AAA64352
11	1195.4	99.9	1197	3	AHA49533
12	1195.4	99.9	1197	8	ABX95717
13	1195.4	99.9	1197	9	ACA62277
14	1195.4	99.9	1197	12	ADG19756
15	1195.4	99.9	1197	13	ADS88806
16	1195.4	99.9	1197	13	ADU61174
17	1195.4	99.9	1609	4	AAS14575
18	1195.4	99.9	1609	12	ADG19754
19	1195.4	99.9	1609	13	ADQ89079

20	1195.4	99.9	1617	8	ACC49540
21	1195	99.8	1197	6	ABQ81125
22	1194	99.7	1194	13	ADR21326
23	1194	99.7	1194	13	ADT05942
24	1192.2	99.6	1197	4	ADT08840
25	1179.4	98.5	1194	4	ADT07922
26	906.4	75.7	969	10	ADC12677
27	836.4	69.9	1188	13	ADR21328
28	836.4	69.9	1188	13	ADT05944
29	836.4	69.9	1191	3	AAA39340
30	836.4	69.9	1191	6	ABS58354
31	836.4	69.9	1237	8	ABX95718
32	836.4	69.9	1237	9	ACA62278
33	832	69.5	1188	4	AAI66036
34	832	69.5	1188	6	ABS54395
35	832	69.5	1188	13	ADR21330
36	832	69.5	1188	13	ADT05946
37	832	69.5	1191	6	ABQ81126
38	832	69.5	1191	12	ADO30215
39	808.8	67.6	1254	3	AAA64353
40	245	20.5	548	4	AA330775
41	186.8	15.6	1309	8	ABZ42788
42	186.8	15.6	1309	14	ADX25933
43	186.8	15.6	1365	2	AAT79976
44	186.8	15.6	1365	9	ADA09963
45	186.8	15.6	1365	11	ADL80089

ALIGNMENTS

RESULT 1

AAA39343

ID AAA39343 standard; cDNA; 1197 BP.

XX

AC AAA39343;

XX

DT 11-SEP-2000 (first entry)

XX

DE Human G protein-coupled receptor protein hOT7T175 encoding cDNA.

XX

KW G protein-coupled receptor protein; rOT7T175; hOT7T175; tumour;

KW guanine nucleotide binding protein; cytosolic; anti-proliferative;

KW cancer; diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO200024890-A1.

XX

PD 04-MAY-2000.

XX

PF 26-OCT-1999; 99WO-JP005905.

XX

PR 27-OCT-1998; 98JP-00305949.

PR

PR 04-FEB-1999; 99JP-00027710.

PR

PR 04-MAR-1999; 99JP-00057207.

XX

XX 29-SEP-1999; 99JP-00276225.

PA

(TAKE) TAKEDA CHEM IND LTD.

XX

XX Watanabe T, Terao Y, Shintani Y, Ohtaki T, Kanehashi K, Kitada C;

XX

XX WPI; 2000-350732/30.

DR

DR P-PSDB; AAY91094.

XX

XX G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its

PT ligands for treatment of diseases including tumors.

XX

PS Claim 6; Page 105-106; 11app; Japanese.

XX

CC The present sequence encodes a human G protein-coupled receptor protein

CC designated hOT7T175. The G protein-coupled receptor protein has

cytostatic and anti-proliferative activities. The protein and antibodies raised against it are useful in the diagnosis, treatment and prevention of disorders with which the G protein-coupled receptor protein is associated, in particular for inhibition of the proliferation of cancers such as lung, kidney, liver, pancreas, colon, breast and ovary cancer. The protein is also used to identify ligands to it by their ability to bind to all or part of the sequence of the protein and for identifying compounds which affect the binding of the protein to its ligands

XX
SQ Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match 100.0%; Score 1197; DB 3; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACACCGTGGCTACGTCGGACCCCAACGCGTCTCTGGGGGGACACGGCCCTCC 60
Db 1 ATGCACACCGTGGCTACGTCGGACCCCAACGCGTCTCTGGGGGGACACGGCCCTCC 60
QY 61 GGCTGCCCGGGCTGTGGGCCCAACGCGTCTGGACGGCCCAAGTCCCTTCCCGCGGGCGGTG 120
Db 61 GGCTGCCCGGGCTGTGGGCCCAACGCGTCTGGACGGCCCAAGTCCCTTCCCGCGGGCGGTG 120
QY 121 GACGCTGGCTGCTGCGCGCTCTTCTTCCGCGCGCTGATGCTGGGCGCTGTGGGAAC 180
Db 121 GACGCTGGCTGCTGCGCGCTCTTCTTCCGCGCGCTGATGCTGGGCGCTGTGGGAAC 180
QY 181 TCGTGGTCACTACGTCATCTGCGCGCACCAAGCGATGCGACCGTTCCTTAC 240
Db 181 TCGTGGTCACTACGTCATCTGCGCGCACCAAGCGATGCGACCGTTCCTTAC 240
QY 241 ATCGCCAACTGGGGGCCACGGACGTGACCTTCTCTGCTGGTCTTCCCTTACGGCC 300
Db 241 ATCGCCAACTGGGGGCCACGGACGTGACCTTCTCTGCTGGTCTTCCCTTACGGCC 300
QY 301 CTGCTGTACCGCTGCGCGCTGGGTGCTGGCGACTTCATGTGCAAGTTCGTCAACTAC 360
Db 301 CTGCTGTACCGCTGCGCGCTGGGTGCTGGCGACTTCATGTGCAAGTTCGTCAACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTGCCACTCTGACCGCATGAGTGTGACCGC 420
Db 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTGCCACTCTGACCGCATGAGTGTGACCGC 420
QY 421 TGGTACGTGACGGTGTTCCTGTTGGCGCCCTGTCACCGCCGACCGCCGCTGGCGGTG 480
Db 421 TGGTACGTGACGGTGTTCCTGTTGGCGCCCTGTCACCGCCGACCGCCGCTGGCGGTG 480
QY 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTCTGCGCGGGTCTGCGCCCTG 540
Db 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGCGGGTCTGCGCGGGTCTGCGCCCTG 540
QY 541 CACCGCTGTACCGCGCGCGCGCTTCTGCACTGAGGCTTCCCGACGCGCGCGCTG 600
Db 541 CACCGCTGTACCGCGCGCGCGCTTCTGCACTGAGGCTTCCCGACGCGCGCGCTG 600
QY 601 GAGCGCGCTTGGCACTGACAACTGCTGGCGCTGTACTGCTGCGCGCTGCTGCGCAC 660
Db 601 GAGCGCGCTTGGCACTGACAACTGCTGGCGCTGTACTGCTGCGCGCTGCTGCGCAC 660
QY 661 TGGCGCTCTATGCGGGCATGCTGGCGCACCTGGCGGGTCTGCGCGGGTCTGCGCGCG 720
Db 661 TGGCGCTCTATGCGGGCATGCTGGCGCACCTGGCGGGTCTGCGCGGGTCTGCGCGCG 720
QY 721 GCCGATAGCGCGCTGACGGGACGCTGTGCGACAGCGCGAGCGCGCTGCGGGCCAAAG 780
Db 721 GCCGATAGCGCGCTGACGGGACGCTGTGCGACAGCGCGAGCGCGCTGCGGGCCAAAG 780
QY 781 GTCTCGCGCTGTGGCGCGCTGTCTGCTTTCGCGCGCTGTGGGGCCCATTCAG 840
Db 781 GTCTCGCGCTGTGGCGCGCTGTCTGCTTTCGCGCGCTGTGGGGCCCATTCAG 840
QY 841 CTGTTCTCTGGTGTGACGGCGCTGGCGCGCGCTCTCTGCGACCCACGACGCTACGCC 900
Db 841 CTGTTCTCTGGTGTGACGGCGCTGGCGCGCGCTCTCTGCGACCCACGACGCTACGCC 900

841 CTGTTCTCTGGTGTGACGGCGCTGGCGCGCGCTCTCTGCGACCCACGACGCTACGCC 900
901 GCCTACGCGCTTAAGACCTTGGGCTCACTGCAATGCTTACAGAACTCCGCGCTGAACCG 960
901 GCCTACGCGCTTAAGACCTTGGGCTCACTGCAATGCTTACAGAACTCCGCGCTGAACCG 960
961 CTGCTCTACGCTTCTGCGCTTGGGCTTCCGACAGGCTTCCGCGCGCTCTGCGCGCTG 1020
961 CTGCTCTACGCTTCTGCGCTTGGGCTTCCGACAGGCTTCCGCGCGCTCTGCGCGCTG 1020
1021 GCG 1080
1021 GCG 1080
1081 GCGAGCTGCAACCGCTTGGGCTTCCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
1081 GCGAGCTGCAACCGCTTGGGCTTCCGACCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
1141 AGTGGGCTGGCG 1197
1141 AGTGGGCTGGCG 1197

RESULT 2
AAD07921
ID AAD07921 standard; cDNA; 1197 BP.
XX
XX AAD07921;
XX AC
XX AC
DT 03-AUG-2001 (first entry)
XX
DE Human G-protein coupled receptor, AXOR12 cDNA.
XX
KW Human; G-protein coupled receptor; AXOR12; chromosome 19p13.3;
KW microbial infection; human immunodeficiency virus; HIV; sleep disorder;
KW pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; gene therapy;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; anxiety;
KW vomiting; dyskinesia; psychotic disorder; neurological disorder; vaccine;
KW dementia; schizophrenia; depression; delirium; mental retardation; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. .1197
FT /*tag= a
FT /product= "G-protein coupled receptor, AXOR12"
XX
PN WO200142486-A1.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033345.
XX
PR 08-DEC-1999; 99US-00456587.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Elshourbagy N, Shabon U, Michalovich D;
XX WPI; 2001-381703/40.
DR P-PSDB; AAE03544.
XX
XX New G-protein coupled receptor polypeptide, AXOR12, useful for treating
PT microbial infections, cancers, obesity, asthma, diabetes, hypotension,
PT osteoporosis, myocardial infarction and neurological disorders.
XX
XX Claim 2; Page 27; 37pp; English.
XX
XX The present sequence is human G-protein coupled receptor AXOR12 cDNA. The
CC AXOR12 gene is located on human chromosome 19p13.3. AXOR12 protein and

polynucleotide are useful for treating and diagnosing infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, dyskinesias, sleep disorders, psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation. AXOR12 protein and polynucleotide are also useful for screening and structure based designing of antagonists, agonists and inhibitors of AXOR12. The protein is useful in screening assays and to identify membrane bound or soluble receptors. The polynucleotide is useful for chromosome localisation studies, as diagnostic reagents for detecting mutations in associated genes, recombinant production of AXOR12 protein, as valuable tools for tissue expression studies and in gene therapy. AXOR12 protein and polynucleotide are also useful as vaccines

Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match 100.0%; Score 1197; DB 4; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCACACCGTGCGTACGTCCGGACCCCAACGCGTCTCTGGGGGCGCACCGGCCCAACGCGCTCC 60
Db 1 ATGCACACCGTGCGTACGTCCGGACCCCAACGCGTCTCTGGGGGCGCACCGGCCCAACGCGCTCC 60

Qy 61 GCGTCCCGGGGTGTGGGCGCCAAAGCGCTCGAGCGCCAGTCCCTTCGCGCGGGCGGTG 120
Db 61 GCGTCCCGGGGTGTGGGCGCCAAAGCGCTCGAGCGCCAGTCCCTTCGCGCGGGCGGTG 120

Qy 121 GACGCGCTGCTGCGCGCTCTCTTCGCGGCGCTGATGCTGCTGGGCGCTGTGGGGAAC 180
Db 121 GACGCGCTGCTGCGCGCTCTCTTCGCGGCGCTGATGCTGCTGGGCGCTGTGGGGAAC 180

Qy 181 TCGCTGTGTCATCTACGTCTATCTGCGCGCCACAGCGGATCGCGACCGGTGACCAACTTCTAC 240
Db 181 TCGCTGTGTCATCTACGTCTATCTGCGCGCCACAGCGGATCGCGACCGGTGACCAACTTCTAC 240

Qy 241 ATGCGCAACCTGGCGGCGACGAGCGTACCTTCCTCTGCTGCTGCGTCCCTTCAACGCGC 300
Db 241 ATGCGCAACCTGGCGGCGGACGAGCGTACCTTCCTCTGCTGCTGCGTCCCTTCAACGCGC 300

Qy 301 CTGCTGTACCGCTGCGCGGTGGTGTGGGCGACTTCATGTGCAAGTTCGTCAACTAC 360
Db 301 CTGCTGTACCGCTGCGCGGTGGTGTGGGCGACTTCATGTGCAAGTTCGTCAACTAC 360

Qy 361 ATCCAGCAGGCTCGGTGAGGCGCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGCG 420
Db 361 ATCCAGCAGGCTCGGTGAGGCGCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGCGC 420

Qy 421 TGGTACGTGACGCTGTTCCGCTTGGCGGCTTGCACCGCGCACCGCGCTGCGCGCTG 480
Db 421 TGGTACGTGACGCTGTTCCGCTTGGCGGCTTGCACCGCGCACCGCGCTGCGCGCTG 480

Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGCGGTGTCTGCGCGGCTGCTGCGCGCTG 540
Db 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGCGGTGTCTGCGCGGCTGCTGCGCGCTG 540

Qy 541 CACCGCTGTACCGCGGCGCGCGCTTACTGCACTGAGGCGCTTCCCGCAGCGCGCGCGCTG 600
Db 541 CACCGCTGTACCGCGGCGCGCGCTTACTGCACTGAGGCGCTTCCCGCAGCGCGCGCGCTG 600

Qy 601 GAGCGCGCTTCGCACTGACAACTGTGCGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GAGCGCGCTTCGCACTGACAACTGTGCGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Qy 661 TCGCGCTGCTATGCGGCGCATGTGCGCCACCTGGGCGGGTGGCGTGGCGCGCGCGCGC 720
Db 661 TCGCGCTGCTATGCGGCGCATGTGCGCCACCTGGGCGGGTGGCGTGGCGCGCGCGCGC 720

Qy 721 GCCGATAGCGCCCTGCGAGGGGACGGTCTGTGCAGAGCGCGAGCGCGTCTCGGGCCAAAG 780
Db 721 GCCGATAGCGCCCTGCGAGGGGACGGTCTGTGCAGAGCGCGAGCGCGTCTCGGGCCAAAG 780

Qy 781 GTCTCGCGGCTGTGTGGGCGCGTGGTCTGTCTTTCGCGCGCTGTGGGGGCGCCATCCAG 840
Db 781 GTCTCGCGGCTGTGTGGGCGCGTGGTCTGTCTTTCGCGCGCTGTGGGGGCGCCATCCAG 840

Qy 841 CTGTCTCTGTGTGTGCGAGGCGCTGGGCGCGCGCGCGCTCTGGGCACCCACGAGCTACGCGC 900
Db 841 CTGTCTCTGTGTGTGCGAGGCGCTGGGCGCGCGCGCGCTCTGGGCACCCACGAGCTACGCGC 900

Qy 901 GCCTACGCGCTTAAGACCTTGGGCTCACTGTGATGTCTTACAGCAACTCCGCGCTGAACCG 960
Db 901 GCCTACGCGCTTAAGACCTTGGGCTCACTGTGATGTCTTACAGCAACTCCGCGCTGAACCG 960

Qy 961 CTGCTCTACGCGCTTCTGGGCTCGCACTTCGAGAGCGCTTCCGCGCGCTGTGCGCGCTGC 1020
Db 961 CTGCTCTACGCGCTTCTGGGCTCGCACTTCGAGAGCGCTTCCGCGCGCTGTGCGCGCTGC 1020

Qy 1021 GCG 1080
Db 1021 GCG 1080

Qy 1081 GCGAGCTGCAACCGCTGGGCTCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1081 GCGAGCTGCAACCGCTGGGCTCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140

Qy 1141 AGTGGGCTGGCGCGCGCGCGCGCTGTGCGTCTGTGGGAGGAGCAAGCGCGCTCTCTGA 1197
Db 1141 AGTGGGCTGGCGCGCGCGCGCGCTGTGCGTCTGTGGGAGGAGCAAGCGCGCTCTCTGA 1197

RESULT 3
ABZ42844
ID ABZ42844 standard; DNA; 1197 BP.
XX AC ABZ42844;
XX DT 04-MAR-2003 (first entry)
XX DE Human G protein-coupled receptor GPR54 nucleotide SEQ ID NO:476.
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX OS Homo sapiens.
XX PN WO200261087-A2.
XX PD 08-AUG-2002.
XX PF 19-DEC-2001; 2001WO-US050107.
XX PR 19-DEC-2000; 2000US-0257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
DR P-PSDB; ABP81995.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors

21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0356714P.
20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
(EOSB-) EOS BIOTECHNOLOGY INC.
Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
WPI; 2003-468649/44.
P-PSDB; ADN39430.
Determining the presence or absence of a pathological cell in a patient,
useful for diagnosing, prognosing or treating cancer, comprises detecting
a nucleic acid in a biological sample.
Claim 8; SEQ ID NO A29; 1385pp; English.
The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularisation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a nucleic acid sequence of the invention.
Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;
Query Match 100.0%; Score 1197; DB 11; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTAGCTCGGACCCAAACGGCTCTCTGGGGGGACCGGCAACGGCTCC 60
DB 1 ATGCACACCGTGGCTAGCTCGGACCCAAACGGCTCTCTGGGGGGACCGGCAACGGCTCC 60
QY 61 GGTGCCCCGGGTGTGGGGCCAAACGGCTCTCGGACGGCCAGTCCCTTCGCGCGGGCGGTG 120
DB 61 GGTGCCCCGGGTGTGGGGCCAAACGGCTCTCGGACGGCCAGTCCCTTCGCGCGGGCGGTG 120
QY 121 GAGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
DB 121 GAGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
QY 181 TGGCTGGCTATCTACCTATCTGCGGCCCAAGCGCGATCGGACCGGTGACCACTTCTAC 240
DB 181 TGGCTGGCTATCTACCTATCTGCGGCCCAAGCGCGATCGGACCGGTGACCACTTCTAC 240
QY 241 ATGCCCAACCTGGCGGCCAGGACGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

241 ATGCCCAACCTGGCGGCCAGGACGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 CTGCTGTATACCGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
DB 301 CTGCTGTATACCGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
QY 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTCACCTCTGACCGCCATGAGTGTGACCGC 420
DB 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTCACCTCTGACCGCCATGAGTGTGACCGC 420
QY 421 TGGTACGTACCGGTCTCCGTTGCGCGCCCTGCAACCGCGCACCGCCCGCTGGCGCTG 480
DB 421 TGGTACGTACCGGTCTCCGTTGCGCGCCCTGCAACCGCGCACCGCCCGCTGGCGCTG 480
QY 481 GCTGTACCGCTCAGCATCTGGGTAGGCTCTGCGGGGGGTGCTGCGCGCGGTGCTGCGCCCTG 540
DB 481 GCTGTACCGCTCAGCATCTGGGTAGGCTCTGCGGGGGGTGCTGCGCGCGGTGCTGCGCCCTG 540
QY 541 CACCGCTGTACCGCGCGCGCGCTTACGTGAGGGCTTCCCGAGCGCGCTTCCCGAGCGCGCCCTG 600
DB 541 CACCGCTGTACCGCGCGCGCGCTTACGTGAGGGCTTCCCGAGCGCGCTTCCCGAGCGCGCCCTG 600
QY 601 GAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 GAGCGCGCTTGGCACTGTACAACTGCTGGCGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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DB 661 TGGCGCTGTATGCGGCCATGCTGCGGCCACCTTGGCGCGGTGCTGCGCGCGGTGCTGCGCCCTG 720
QY 721 GCCGATAGCGCTTACAGGGGCGAGTGTGCGAGCGCGGAGGCGCGCTGCGGGCCGACG 780
DB 721 GCCGATAGCGCTTACAGGGGCGAGTGTGCGAGCGCGGAGGCGCGCTGCGGGCCGACG 780
QY 781 GTCTCGCGCTGCTGGCGCGCTGCTGCTGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 GTCTCGCGCTGCTGGCGCGCTGCTGCTGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 GTGTTCTGTGCTGACGGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCG 900
DB 841 GTGTTCTGTGCTGACGGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCG 900
QY 901 GCCTACGCGCTTAGACCTGGGCTCAGTGTCTTACAGCACTCCGCGCTGGAACCG 960
DB 901 GCCTACGCGCTTAGACCTGGGCTCAGTGTCTTACAGCACTCCGCGCTGGAACCG 960
QY 961 CTGCTCTACGCGCTTCTCGGGCTCGCACTTCGAGACAGGCTTTCGCGCGGTCTGCGCCCTG 1020
DB 961 CTGCTCTACGCGCTTCTCGGGCTCGCACTTCGAGACAGGCTTTCGCGCGGTCTGCGCCCTG 1020
QY 1021 GCG 1080
DB 1021 GCG 1080
QY 1081 GCGGAGCTGACCGCTGGGTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
DB 1081 GCGGAGCTGACCGCTGGGTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1141 AGTGGGCTGGCGCGCGCGCGCGCTGTCCTTCTGCGGGGAGGACCAACCGCCCTCTCTGA 1197
DB 1141 AGTGGGCTGGCGCGCGCGCGCGCTGTCCTTCTGCGGGGAGGACCAACCGCCCTCTCTGA 1197

RESULT 5
ADN39504
ID ADN39504 standard; cDNA; 1197 BP.
XX
AC ADN39504;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A104.

[illegible]

QY 1081 GCGAGCTGCACCGCTGGGTCCACCCGCGCCCCCGCCAGCGGCGCAGAAAGCCAGGAGC 1140
 Db 1081 GCGAGCTGCACCGCTGGGTCCACCCGCGCCCCCGCCAGCGGCGCAGAAAGCCAGGAGC 1140
 QY 1141 AGTGGCTGGCGCGCGCGGTGTCGTCCTGGGGAGGACAAAGCCCTCTCTGA 1197
 Db 1141 AGTGGCTGGCGCGCGCGGTGTCGTCCTGGGGAGGACAAAGCCCTCTCTGA 1197

RESULT 6

ADL91584

ID ADL91584 standard; cDNA; 1197 BP.

AC ADL91584;

DT 17-JUN-2004 (first entry)

DE Human immune-related polypeptide PRO47351-encoding cDNA, SEQ ID NO:99.

KW Human; PRO; activated T cell; immune-related; drug screening; detection;
 KW stimulation; immune response; stimulation; diagnosis; immune-mediated skin disease;
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; spondyloarthritis; systemic sclerosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome;
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KW immune-mediated renal disease; demyelinating disease;
 KW idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;
 KW chronic active hepatitis; primary biliary cirrhosis;
 KW granulomatous hepatitis; sclerosing cholangitis;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW Whipple's disease; autoimmune skin disease; immune-mediated skin disease;
 KW bullous skin disease; erythema multiforme; contact dermatitis; psoriasis;
 KW allergic disease; asthma; allergic rhinitis; atopic dermatitis;
 KW food hypersensitivity; urticaria; eosinophilic pneumonia;
 KW idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;
 KW transplantation associated disease; graft rejection;
 KW graft-versus-host disease; immunosuppressive; dermatological;
 KW hepatotropic; nephrotropic; antidiabetic; antiaesthetic; antipsoriatic;
 KW antiallergic; antianemic; antiarteriosclerotic; antiarthritic;
 KW neuroprotective; respiratory; antiinflammatory; gene therapy; gene; ss.

OS Homo sapiens.

PN WO2004024072-A2.

XX 25-MAR-2004.

XX 10-SEP-2003; 2003WO-US028317.

XX 11-SEP-2002; 2002US-0410340P.

XX (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

XX Williams PM, Wood WI, Wu TD;

XX WPI: 2004-329384/30.

DR P-PSDB; ADU91585.

XX New PRO nucleic acid, useful for preparing a composition for diagnosing
 PT or treating an immune related disorder, e.g., systemic lupus
 PT erythematosus in a mammal.

PS Claim 2; SEQ ID NO 99; 199pp; English.

XX

CC The invention relates to isolated human immune-related polypeptides

CC (designated PRO) and nucleic acids (ADL91486-ADL91587). The PRO
 CC polypeptides are overexpressed in CD4+ T cells activated by anti-CD3/ICAM

CC -1 or anti-CD3/anti-CD28 antibodies compared with resting T cells and are
 CC useful as diagnostic markers and therapeutic targets for immune

CC disorders. The invention also relates to sequences at least 80% identical

CC to the PRO nucleic acid and polypeptide sequences of the invention;
 CC recombinant vectors and host cells comprising a PRO nucleic acid; a
 CC method for the recombinant production of a PRO polypeptide; antibodies
 CC against a PRO polypeptide; fusion proteins comprising a PRO polypeptide;
 CC methods of screening for compounds which modulate PRO polypeptide
 CC activity or expression; a method for detecting a PRO polypeptide; a
 CC method of detecting an immune response in a mammal; and methods for
 CC stimulating an immune response in a mammal; and methods for diagnosing
 CC and treating immune-related disorders. PRO polypeptides and nucleic acids
 CC are useful in the diagnosis and treatment of immune-related disorders
 CC such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic
 CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease,
 CC infectious or autoimmune chronic active hepatitis, primary biliary
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
 CC autoimmune or immune-mediated skin disease, bullous skin disease,
 CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
 CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,
 CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
 CC transplantation associated disease, graft rejection or graft-versus-host-
 CC disease. The present sequence represents cDNA encoding a human immune-
 CC related PRO polypeptide of the invention.

XX SQ Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 1197; DB 12; Length 1197;

Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACACCGGTGGTACGTCCGGACCCCAACGCGTCTCGGGGGGACCGCGCAACGCTCC 60

Db 1 ATGCACACCGGTGGTACGTCCGGACCCCAACGCGTCTCGGGGGGACCGCGCAACGCTCC 60

QY 61 GGCTGCCCGGGCTGTGGCGCCCAACGCTTCGACACGGCCAGTCCCTTCGCGCGGGCGGTG 120

Db 61 GGCTGCCCGGGCTGTGGCGCCCAACGCTTCGACACGGCCAGTCCCTTCGCGCGGGCGGTG 120

QY 121 GACGCTGGCTCGTGGCGCTCTTCTTTCGCGCGCTGTAGTCTGCTGGGCTGTGGGGAAC 180

Db 121 GACGCTGGCTCGTGGCGCTCTTCTTTCGCGCGCTGTAGTCTGCTGGGCTGTGGGGAAC 180

QY 181 TCGTGGTCACTACGTCACTGCGCGCAACGCGGATGCGGACCGTGACCAACTTCTAC 240

Db 181 TCGTGGTCACTACGTCACTGCGCGCAACGCGGATGCGGACCGTGACCAACTTCTAC 240

QY 241 ATCGCAACCTGGGGGCCACGAGTGACCTTCTCTGTGTGGTGTCCCTTTCAGCGCC 300

Db 241 ATCGCAACCTGGGGGCCACGAGTGACCTTCTCTGTGTGGTGTCCCTTTCAGCGCC 300

QY 301 CTGCTGTACCCGCTGCCCGGCTGGGTCTGGCGGCACTTCAATGTGCAAGTTCGTCAACTAC 360

Db 301 CTGCTGTACCCGCTGCCCGGCTGGGTCTGGCGGCACTTCAATGTGCAAGTTCGTCAACTAC 360

QY 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTGCCACTCTGACCGGCATGAGTGTGGACGCG 420

Db 361 ATCCAGCAGGTCTCGGTGACGCCACGCTGTGCCACTCTGACCGGCATGAGTGTGGACGCG 420

QY 421 TGGTACGTGACGGGTGTTCCTGCGGCTTCGACCGCCGCGCGCGCTTGGCGGTG 480

Db 421 TGGTACGTGACGGGTGTTCCTGCGGCTTCGACCGCCGCGCGCGCTTGGCGGTG 480

QY 481 GCTGTGACGCTCAGCATCTGGGTAGGTCTCGCGGGTGTCTGCGCGGTGTCTCGCCCTG 540

Db 481 GCTGTGACGCTCAGCATCTGGGTAGGTCTCGCGGGTGTCTGCGCGGTGTCTCGCCCTG 540

QY 541 CACCGCTGTCAACCCCGCGCGCGCTTACTGCAATGAGGGCTTTCCTCCAGCGCGCGCTG 600


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Db 541 CACCGCCCTGTACCCGCGCGCGCCCTACTGCACTGAGGGCTTCCCCAGCGCGCCCTG 600
Qy 601 GAGCGCGCCTTTCGCACTGTACAACTGCTGGCGCTGTACCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GAGCGCGCCTTTCGCACTGTACAACTGCTGGCGCTGTACCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 TCGCGCTGCTATGCGCGCATGCTGCGCACCTGCGCCCGGGTTCGCGTGGCGCCCGCGCC 720
Db 661 TCGCGCTGCTATGCGCGCATGCTGCGCACCTGCGCCCGGGTTCGCGTGGCGCCCGCGCC 720
Qy 721 GCCGATAGCGCCCTCAGCGGCGAGTGTGCGCAGAGCGCGAGCGCGCTGGCGGCCAAG 780
Db 721 GCCGATAGCGCCCTCAGCGGCGAGTGTGCGCAGAGCGCGAGCGCGCTGGCGGCCAAG 780
Qy 781 GTCTCGCGCTGTGTCGCGCGCTGTGCTCTTTCGCGCGCTGTGTCGCGGCCCATCCAG 840
Db 781 GTCTCGCGCTGTGTCGCGCGCTGTGCTCTTTCGCGCGCTGTGTCGCGGCCCATCCAG 840
Qy 841 CTGTTCTCTGCTGCTGCGCGCTGCGCGCGCGCGCGCGCTCTGCGCACCCACGAGCTACGCC 900
Db 841 CTGTTCTCTGCTGCTGCGCGCTGCGCGCGCGCGCGCGCTCTGCGCACCCACGAGCTACGCC 900
Qy 901 GCTACGCGCTTAAAGACCTGGGCTCAGTGCATGCTCTACAGCACTCCGCGCTGAACCCG 960
Db 901 GCTACGCGCTTAAAGACCTGGGCTCAGTGCATGCTCTACAGCACTCCGCGCTGAACCCG 960
Qy 961 CTGCTCTACGCTTCTCGGCTGCGCACTTCGACAGGCTTTCGCGCGCGTCTGCGCCCTGC 1020
Db 961 CTGCTCTACGCTTCTCGGCTGCGCACTTCGACAGGCTTTCGCGCGCGTCTGCGCCCTGC 1020
Qy 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Qy 1081 GCGGAGCTGCAACGCTGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140
Db 1081 GCGGAGCTGCAACGCTGGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140
Qy 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGTCTGCGGGGAGGCAACGCGCCCTCTCTGA 1197
Db 1141 AGTGGGCTGGCGCGCGCGCGCTGTGCGTCTGCGGGGAGGCAACGCGCCCTCTCTGA 1197

RESULT 7
ID ADO29925
AC ADO29925;
XX ADO29925;
XX ADO29925;
DT 29-JUL-2004 (first entry)
DE Human GPCR GPR54 polynucleotide, SEQ ID NO:1027.
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antiamebic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
OS Homo sapiens.
XX
XX WO2004040000-A2.
PN
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XX PD 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX PF 09-SEP-2002; 2002US-0409303P.
XX PR 09-APR-2003; 2003US-0461329P.
XX PA (PRIM-) PRIMAL INC.
XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR P-PSDB; ADO29412.
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 1027; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders; blood disorders (e.g.,
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
XX nucleic acid of the invention. Note: The full sequence data for this
XX patent did not form part of the printed specification; those sequences
XX not shown were obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;
Qy Query Match 100.0%; Score 1197; DB 12; Length 1197;
Best Local Similarity 100.0%; Pred. No. 2.2e-167;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACACCGTGGCTAGCTCGGACCCCAACGCGTCTGGGGGGGACCGCCCAACGCGCTCC 60
Db 1 ATGCACACCGTGGCTAGCTCGGACCCCAACGCGTCTGGGGGGGACCGCCCAACGCGCTCC 60
Qy 61 GGCTGCCCGGCTGTGGCGCCCAACGCGTCTGGAGCGGCCAGTCCCTTGGCGGCGGCGGTG 120
Db 61 GGCTGCCCGGCTGTGGCGCCCAACGCGTCTGGAGCGGCCAGTCCCTTGGCGGCGGCGGTG 120
Qy 121 GAGCGCTGGCTGCTGCGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGCGCTGGTGGGGAAC 180
Db 121 GAGCGCTGGCTGCTGCGCGCTCTTCTTCGCGCGCTGATGCTGCTGGGCGCTGGTGGGGAAC 180
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Db 241 ATCGCCAACTGGCGGCCACGAGCTGACCTTCCTCTGTGCTGGCTCCCTTACGGCC 300
Qy 301 CTGCTGTACCGCTGCCCGCTGGGTGTGGCGGACTTCATGTGCAAGTTTCGTCAACTAC 360
Db 301 CTGCTGTACCGCTGCCCGCTGGGTGTGGCGGACTTCATGTGCAAGTTTCGTCAACTAC 360
Qy 361 ATCCAGCAGGCTCTGGTGTGCGGCCACGCTGTGCCACTCTGACCGCATAGTGTGGACCGC 420
Db 361 ATCCAGCAGGCTCTGGTGTGAGGCCACGCTGTGCCACTCTGACCGCATAGTGTGGACCGC 420
Qy 421 TGGTACGTGACGGTGTTCCTGGTGTGCGCGCCCTTGACACCGCCCGCTGGCGCTG 480
Db 421 TGGTACGTGACGGTGTTCCTGGTGTGCGCGCCCTTGACACCGCCCGCTGGCGCTG 480
Qy 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGTGTGTGCGCGGTGTGTGCGCCGTG 540
Db 481 GCTGTACGCTCAGCATCTGGGTAGGCTCTGCGGCGGTGTGTGCGCGGTGTGTGCGCCGTG 540
Qy 541 CACCGCCTGTACCGCGCGCGCGCTACTGCACTGAGTGTGGCTTCCCGCGCGCGCTG 600
Db 541 CACCGCCTGTACCGCGCGCGCGCTACTGCACTGAGTGTGGCTTCCCGCGCGCGCTG 600
Qy 601 GAGCGCGCTTCGCACTGTACAACTGCTGGCGCTGTACCTGCTGCGCTGTGCGCCACC 660
Db 601 GAGCGCGCTTCGCACTGTACAACTGCTGGCGCTGTACCTGCTGCGCTGTGCGCCACC 660
Qy 661 TCGCCTGTATGCGGCCATGCTGCGCCACCTGTGGCGCGGTGTGCGCGCGCGCGCTG 720
Db 661 TCGCCTGTATGCGGCCATGCTGCGCCACCTGTGGCGCGGTGTGCGCGCGCGCGCTG 720
Qy 721 GCGGATAGCGCCTGACGGGCGAGTGTGCGAGAGCGCGAGCGCGCTGCGGGCCAG 780
Db 721 GCGGATAGCGCCTGACGGGCGAGTGTGCGAGAGCGCGAGCGCGCTGCGGGCCAG 780
Qy 781 GTCTCGCGCTGGTGTGCGCGCGCTGTCTGCTCTTCGCGCGCTGTGCGGCGCCATCCAG 840
Db 781 GTCTCGCGCTGGTGTGCGCGCGCTGTCTGCTCTTCGCGCGCTGTGCGGCGCCATCCAG 840
Qy 841 CTGTTCTGTGTGCTCAGCGCTGTGGCGCCCGCGGCTCTGTGCAACCCACGAGCTACGCC 900
Db 841 CTGTTCTGTGTGCTCAGCGCTGTGGCGCCCGCGGCTCTGTGCAACCCACGAGCTACGCC 900
Qy 901 GCCTACGCGCTTAAGACTTGGGCTCAGTGCATGTCTTACAGCACTTCGCGCTGAACCG 960
Db 901 GCCTACGCGCTTAAGACTTGGGCTCAGTGCATGTCTTACAGCACTTCGCGCTGAACCG 960
Qy 961 CTGCTCTACGCTTCTTGGGCTCGCACTTCGACAGGCTTTCGCGCGGTGTGCGCCCTGC 1020
Db 961 CTGCTCTACGCTTCTTGGGCTCGCACTTCGACAGGCTTTCGCGCGGTGTGCGCCCTGC 1020
Qy 1021 GCG 1080
Db 1021 GCG 1080
Qy 1081 GCGGAGCTGACCGCTGGGTTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1081 GCGGAGCTGACCGCTGGGTTCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Qy 1141 AGTGGGCTGGCGCGCGCGCGGTGTGCGTCTTGGGGGAGGCAAGCGCCCTCTCTGA 1197
Db 1141 AGTGGGCTGGCGCGCGCGCGGTGTGCGTCTTGGGGGAGGCAAGCGCCCTCTCTGA 1197

RESULT 9

ID ADZ68968
XX ADZ68968 standard; cDNA; 1197 BP.
AC ADZ68968;
XX
DT 14-JUL-2005 (first entry)
DE Human G protein coupled receptor 54 (GPR54) cDNA.
XX

uropathic; substrate inhibition; pharmaceutical; genitourinary disease;
bladder disease; micturition disorder; prostate hyperplasia; cytostatic;
androgyny; gynecology and obstetrics; G protein coupled receptor 54;
GPR54; Kiss1; gene; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..1197
FT /*tag= a
FT /product= "GPR54"
XX /note= "G protein coupled receptor 54"

W02005040833-A1.

06-MAY-2005.

06-OCT-2004; 2004WO-EP011250.

21-OCT-2003; 2003EP-00023850.

(FARB) BAYER HEALTHCARE AG.

Yanamoto N, Matsumoto H, Hayashi F, Tajimi M;

WPI; 2005-355924/36.

P-PSDB; ADZ68969.

Screening for agents that decrease the activity of human metastin
recognizing receptors, for treating urological disorders, by contacting a
test compound with human metastin recognizing receptor polypeptide or
polynucleotide.

Example 1; SEQ ID NO 1; 65pp; English.

The invention describes a method of screening for agents, which decrease
the activity of human metastin recognizing receptor comprising:
contacting a test compound with any human metastin recognizing receptor
polypeptide or polynucleotide; and detecting binding of the test compound
to the human metastin recognizing receptor polypeptide or polynucleotide,
where a test compound which binds to the polypeptide or polynucleotide is
identified as a potential therapeutic agent for decreasing the activity
of a human metastin recognizing receptor and for treating urological
disorders. Also described are: a method of screening for agents which
regulate the activity of a human metastin recognizing receptor, by
contacting a test compound with a human metastin recognizing receptor
polypeptide; and detecting a human metastin recognizing receptor activity
of the polypeptide, where a test compound which decreases the human
metastin recognizing receptor activity of the polypeptide is identified
as a potential therapeutic agent for decreasing the activity of the human
metastin recognizing receptor and useful to treat urological disorders; a
method of reducing the activity of human metastin recognizing receptors,
comprising contacting a cell with a reagent which specifically binds to
human metastin recognizing receptor polynucleotide or a human metastin
recognizing receptor polypeptide, where the activity of human metastin
recognizing receptor is reduced and a urological disorder is ameliorated;
a reagent that modulates the activity of a human metastin recognizing
receptor polypeptide or polynucleotide, where the reagent is identified
by the method cited above; and a pharmaceutical composition for the
treatment of urological disorders, comprising: the reagent, and a
carrier. The methods and compositions are useful for treating urological
disorder, such as detrusor overactivity (overactive bladder), urinary
incontinence, neurogenic detrusor overactivity (detrusor hyperreflexia),
idiopathic detrusor overactivity (detrusor instability), benign prostatic
hyperplasia, and lower urinary tract symptoms. The reagent is useful in
the preparation of a medicament for modulating the activity of human
metastin recognizing receptor in a urological disorder. This sequence
encodes human G protein coupled receptor 54 (GPR54), a metastin
recognising receptor.

Sequence 1197 BP; 131 A; 481 C; 385 G; 200 T; 0 U; 0 Other;

Query Match 100.0%; Score 1197; DB 14; Length 1197;

Qy	1	ATGCACACCGTGGCTACGCTCCGGACCCAAACGCGTCTCTGGGGGGACACGGCCAAACGCTTCC	60
Db	1	ATGCACACCGTGGCTACGCTCCGGACCCAAACGCGTCTCTGGGGGGACACGGCCAAACGCTTCC	60
Qy	61	GGCTGCCCGGCTGTGGGGCCAAACGCTCTGGACCGGCCAGTCCCTTTCGCGCGGGGCGCGT	120
Db	61	GGCTGCCCGGCTGTGGGGCCAAACGCTCTGGACCGGCCAGTCCCTTTCGCGCGGGGCGCGT	120
Qy	121	GACGCTGGCTGTGTCGCGCTCTTCTTTCGCGCGCTGATGTGCTGGGCTTGGTGGGAAC	180
Db	121	GACGCTGGCTGTGTCGCGCTCTTCTTTCGCGCGCTGATGTGCTGGGCTTGGTGGGAAC	180
Qy	181	TGCTGTGGTCACTACGTACATCTGCGGCCACAAAGCCGATGCGGAACGTTCTTAC	240
Db	181	TGCTGTGGTCACTACGTACATCTGCGGCCACAAAGCCGATGCGGAACGTTCTTAC	240
Qy	241	ATGCCAACCTGGCGGGCCACGGACGTGACCTTCTCTGTGCTGTGCTGCTGCTGCTGCGCC	300
Db	241	ATGCCAACCTGGCGGGCCACGGACGTGACCTTCTCTGTGCTGTGCTGCTGCTGCTGCGCC	300
Qy	301	CTGCTGTACCGCTGCCCGGCTGGGTGTGGGGCACTTCAATGTGCAAGTTGTTCAACTAC	360
Db	301	CTGCTGTACCGCTGCCCGGCTGGGTGTGGGGCACTTCAATGTGCAAGTTGTTCAACTAC	360
Qy	361	ATCCAGCAGGTCTCGGTGCAGGCCACAGTGTGCCACTCTGACCGGCCATGAGTGTGACCGC	420
Db	361	ATCCAGCAGGTCTCGGTGCAGGCCACAGTGTGCCACTCTGACCGGCCATGAGTGTGACCGC	420
Qy	421	TGTTACCTGACGGTGTTCCTGTTGGGGCCCTGACCGCCGCGCACGCGCCCGCTGGCGCTG	480
Db	421	TGTTACCTGACGGTGTTCCTGTTGGGGCCCTGACCGCCGCGCACGCGCCCGCTGGCGCTG	480
Qy	481	GCTGTACGCTCAGCATCTGGTATGGTCTGTGCGCGGTGTCTGCGCGGTGCTCGCCCTG	540
Db	481	GCTGTACGCTCAGCATCTGGTATGGTCTGTGCGCGGTGTCTGCGCGGTGCTCGCCCTG	540
Qy	541	CACCGCTGTACACCGGGCCGGCGCTACTGTGAGTGAGGCTTCCCAGCGCGCGCTG	600
Db	541	CACCGCTGTACACCGGGCCGGCGCTACTGTGAGTGAGGCTTCCCAGCGCGCGCTG	600
Qy	601	GAGCGCGCTTCGACATGTACAACTGTGCGCGCTGTACCTGTGCGCGCTGCTCGCCACC	660
Db	601	GAGCGCGCTTCGACATGTACAACTGTGCGCGCTGTACCTGTGCGCGCTGCTCGCCACC	660
Qy	661	TGGCCTGTGATGCGGCATGCTCGGCACTGTGGCCGGGTTCGCGTTCGCGCCCGCC	720
Db	661	TGGCCTGTGATGCGGCATGCTCGGCACTGTGGCCGGGTTCGCGTTCGCGCCCGCC	720
Qy	721	GCCGATAGCGCCGTGACGGGACGTCGTGCGACAGCGCGCAGCGCGGTGCGGGCCAG	780
Db	721	GCCGATAGCGCCGTGACGGGACGTCGTGCGACAGCGCGCAGCGCGGTGCGGGCCAG	780
Qy	781	GTCTTCGCGGCTGTGGGGCGCTGGTCTGTCTTTCGCGCGCTGTGGGGCCCATCCAG	840
Db	781	GTCTTCGCGGCTGTGGGGCGCTGGTCTGTCTTTCGCGCGCTGTGGGGCCCATCCAG	840
Qy	841	CTGTTCCTGTGTGTCAGAGCGCTGGGCCCGCGGGCTCTGTGGCAACCAACGAGCTAGCC	900
Db	841	CTGTTCCTGTGTGTCAGAGCGCTGGGCCCGCGGGCTCTGTGGCAACCAACGAGCTAGCC	900
Qy	901	GCCTACCGGCTTAAGACTGGGCTCACTGTGATGTCCTACAGCACTCGCGCTGAACCG	960
Db	901	GCCTACCGGCTTAAGACTGGGCTCACTGTGATGTCCTACAGCACTCGCGCTGAACCG	960
Qy	961	CTGCTCTACGCTTCTCTGGGCTCGCACTTTCGACAGGCTTTCGCGCGCTGTGCGCTG	1020
Db	961	CTGCTCTACGCTTCTCTGGGCTCGCACTTTCGACAGGCTTTCGCGCGCTGTGCGCTG	1020
Qy	1021	GCGCGCGCGCTCCCGCGCGCCCGCGCGCGCGGACCTGTGGACCCCGCAGGCCCAAC	1080

Query Match		99.9%;	Score 1195.4;	DB 3;	Length 1197;
Best Local Similarity		99.9%;	Pred. No. 3.7e-167;		
Matches 1196;		Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	ATGCACACCGTGGCTACGTCGGAGCCCAACCGTCTCTGGGGGGACACCGGCCCAACGCCCTCC	60		
Db	1	ATGCACACCGTGGCTACGTCGGAGCCCAACCGTCTCTGGGGGGACACCGGCCCAACGCCCTCC	60		
Qy	61	GGCTCCCGGGCTGTGGGGCCCAACCGCTCGAGAGCCCAAGTCTTTCGCGGGGCGGTG	120		
Db	61	GGCTCCCGGGCTGTGGGGCCCAACCGCTCGAGAGCCCAAGTCTTTCGCGGGGCGGTG	120		
Qy	121	GAGCGCTGCGTCTGCGCGCTCTTCTTCGCGGGCGTGATGCTGCTGGGCGCTGTGGGGAAC	180		
Db	121	GAGCGCTGCGTCTGCGCGCTCTTCTTCGCGGGCGTGATGCTGCTGGGCGCTGTGGGGAAC	180		
Qy	181	TGCTGTGTCATCTACGTCATCTGCGGCCCAAGCCGATGCGGACCGTGACCAACTTCTAC	240		
Db	181	TGCTGTGTCATCTACGTCATCTGCGGCCCAAGCCGATGCGGACCGTGACCAACTTCTAC	240		
Qy	241	ATCGCCAACTGGCGGCCGACGAGCTGACCTTCTCTGCTGTGCTGCTTCAACGCC	300		
Db	241	ATCGCCAACTGGCGGCCGACGAGCTGACCTTCTCTGCTGTGCTGCTTCAACGCC	300		
Qy	301	CTGCTGTACCGCTGCGCGGCTGGTGTGGGCACTTCATGTGCAAGTTGTCACACTAC	360		
Db	301	CTGCTGTACCGCTGCGCGGCTGGTGTGGGCACTTCATGTGCAAGTTGTCACACTAC	360		
Qy	361	ATCCAGCAGGTCGCTGTCAGGCCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGC	420		
Db	361	ATCCAGCAGGTCGCTGTCAGGCCACGCTGTGCACTCTGACCGCCATGAGTGTGACCGC	420		
Qy	421	TGGTACGTACGCTGTTCCGCTTGGCGCCCTGTGACCGCGACGCCCGCTGCGCGTG	480		
Db	421	TGGTACGTACGCTGTTCCGCTTGGCGCCCTGTGACCGCGACGCCCGCTGCGCGTG	480		
Qy	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGGGGTGTCTGCGCGGTGCTCGCCCTG	540		
Db	481	GCTGTACGCTCAGCATCTGGGTAGGCTCTGGGGGGTGTCTGCGCGGTGCTCGCCCTG	540		
Qy	541	CACCGCTGTACCGCGCGCGCGCTTACTGTCAGTGAGGCTTCTCCCGAGCGCGGCCCTG	600		
Db	541	CACCGCTGTACCGCGCGCGCGCTTACTGTCAGTGAGGCTTCTCCCGAGCGCGGCCCTG	600		
Qy	601	GAGCGCGCTTGGCACTGTAACCTGTGGCGCTGTACCTGTGCGCGCTGCTGCGCAC	660		
Db	601	GAGCGCGCTTGGCACTGTAACCTGTGGCGCTGTACCTGTGCGCGCTGCTGCGCAC	660		
Qy	661	TGCGCTGTATGCGGSCATGTCGCGCACCTGGGCGGGTCTGCGCGCGCGCGCGCC	720		
Db	661	TGCGCTGTATGCGGSCATGTCGCGCACCTGGGCGGGTCTGCGCGCGCGCGCGCC	720		
Qy	721	GCGGATAGCGCCTCAGGGGAGGTGTGGCAGAGCGCGAGGCGCGCTGCGGGCCAAG	780		
Db	721	GCGGATAGCGCCTCAGGGGAGGTGTGGCAGAGCGCGAGGCGCGCTGCGGGCCAAG	780		
Qy	781	GTCGCGCGCTGTGGCGCGCTGTCTGTCTTTCGCGCGCTGTGGGGGCCCATTCAG	840		
Db	781	GTCGCGCGCTGTGGCGCGCTGTCTGTCTTTCGCGCGCTGTGGGGGCCCATTCAG	840		
Qy	841	CTGTTCTGTGTGTCAGCGCTGGGCGCCCGGGCTCTCTGGCACCCACGAGCTACGCC	900		
Db	841	CTGTTCTGTGTGTCAGCGCTGGGCGCCCGGGCTCTCTGGCACCCACGAGCTACGCC	900		
Qy	901	GCTACGCGCTTAAGACCTTGGGCTCACTGTCATGTCTTACAGCACTCCGCGCTGAACCCG	960		
Db	901	GCTACGCGCTTAAGACCTTGGGCTCACTGTCATGTCTTACAGCACTCCGCGCTGAACCCG	960		
Qy	961	GTGCTCTAGCGCTTCTGGGCTCGACCTTCGACAGGCGCTTCGCGCGCTGTGCGCTG	1020		
Db	961	GTGCTCTAGCGCTTCTGGGCTCGACCTTCGACAGGCGCTTCGCGCGCTGTGCGCTG	1020		
Qy	1021	GCG	1080		

Db	1021																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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CC arthritis, autoimmune diseases, transplant rejection, graft versus host
 CC disease, bacterial, fungal, protozoan and viral infections, septicemia,
 CC AIDS, pain, psychotic and neurological disorders, including anxiety,
 CC depression, schizophrenia, dementia, mental retardation, memory loss,
 CC epilepsy, locomotor problems, respiratory disorders, asthma, eating/body
 CC weight disorders including obesity, bulimia, diabetes, anorexia, nausea,
 CC hypertension, hypotension, vascular and cardiovascular disorders,
 CC ischaemia, stroke, cancers, ulcers, urinary retention, sexual/
 CC reproductive disorders, circadian rhythm disorders, renal disorders, bone
 CC diseases including osteoporosis, benign prostatic hypertrophy,
 CC gastrointestinal disorders, nasal congestion, allergies, Parkinson's
 CC disease and Alzheimer's disease, and diagnostic assays for such
 CC conditions. The present sequence encodes the human SNORF11 receptor
 xx

Sequence 1197 BP; 130 A; 481 C; 385 G; 201 T; 0 U; 0 Other:

Query Match	99.9%;	Score 1195.4;	DB 9;	Length 1197;	
Best Local Similarity	99.9%;	Pred. No. 3.7e-167;			
Matches 1196;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATGCACACCGTGGCTACGTCGCGAGCCCAACCGTCTCTGGGGGGCGACCGGCCCAACGCCTCC	60		
Db	1	ATGCACACCGTGGCTACGTCGCGAACCCCAACCGGTCTTGGGGGGCGACCGGCCCAACGCCTCC	60		
Qy	61	GGCTGCCCGGGCTGTGGCGGCCCAACCGCTCTGGACGGCCAGTCCCTTCGCGCGGGCGCGTG	120		
Db	61	GGCTGCCCGGGCTGTGGCGGCCCAACCGCTCTGGACGGCCAGTCCCTTCGCGCGGGCGCGTG	120		
Qy	121	GACGCTGGCTCGTGCCTCTTCTTTCGGGGGGCTGATGCTGCTGGCGCTGTGTGGGGAAAC	180		
Db	121	GACGCTGGCTCGTGCCTCTTCTTTCGGGGGGCTGATGCTGCTGGCGCTGTGTGGGGAAAC	180		
Qy	181	TCGCTGTGTCATCTACGTCATCTGCCGCCACAAGCCGATGCGGACCGTGACCAACTTCTTAC	240		
Db	181	TCGCTGTGTCATCTACGTCATCTGCCGCCACAAGCCGATGCGGACCGTGACCAACTTCTTAC	240		
Qy	241	ATCGCCAACTTGGGGGCCACGGAAGTGATGACTTCTCTCTGTGCTGCTGCCCTTCCCTTTCACGGCC	300		
Db	241	ATCGCCAACTTGGGGGGCACGGAAGTGATGACTTCTCTCTGTGCTGCTGCCCTTCCCTTTCACGGCC	300		
Qy	301	CTGCTGTACCCGCTGCCCGGCTGGGTGTGGGGGACTTCACTGTGCAAGTTCGTCAACTAC	360		
Db	301	CTGCTGTACCCGCTGCCCGGCTGGGTGTGGGGGACTTCACTGTGCAAGTTCGTCAACTAC	360		
Qy	361	ATCAGCAGGTCTCGGTGACGGCCACGCTGTGCACCTCTGACCGCCATGAGTGTGACCGCC	420		
Db	361	ATCAGCAGGTCTCGGTGACGGCCACGCTGTGCACCTCTGACCGCCATGAGTGTGACCGCC	420		
Qy	421	TGGTACGTGACGGTGTTCGGTTCGGCGGCTGTGCACCGCGCATCGCGCTGCGGCTG	480		
Db	421	TGGTACGTGACGGTGTTCGGTTCGGCGGCTGTGCACCGCGCATCGCGCTGCGGCTG	480		
Qy	481	GCTGTACGCCCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCGGTGTCTGCCCTTG	540		
Db	481	GCTGTACGCCCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCGGTGTCTGCCCTTG	540		
Qy	541	CACGCGCTGTCAACCGGGCCGCGGCTACTGCACTGAGGCTTCCCCAGCGCGGCTG	600		
Db	541	CACGCGCTGTCAACCGGGCCGCGGCTACTGCACTGAGGCTTCCCCAGCGCGGCTG	600		
Qy	601	GAGCGGCTTTCGACTGTACACTGTGCGCTGTACTGCTGCGCTGTCTGCTGCCAC	660		
Db	601	GAGCGGCTTTCGACTGTACACTGTGCGCTGTACTGCTGCGCTGTCTGCTGCCAC	660		
Qy	661	TGCGCTCTACTATGCGGCCATGCTGCGCACTTGGGCCGGGTGCGCGTGCGCCCGCGGCC	720		
Db	661	TGCGCTCTACTATGCGGCCATGCTGCGCACTTGGGCCGGGTGCGCGTGCGCCCGCGGCC	720		
Qy	721	GCCGATAGCGCCTTCGAGGGGCAAGTGTGCGACAGCGGCGCGCTGCGGGCCAAAG	780		
Db	721	GCCGATAGCGCCTTCGAGGGGCAAGTGTGCGACAGCGGCGCGCTGCGGGCCAAAG	780		
Qy	781	GTCTCGCGGGTGTGTGGGGCGGTGCTCTGCTCTTTCGCGCGCTGTCTGGGGGCCCATCCAG	840		

Db	781		GTCTCGCGGCTGGTGGCGGCGTGGTCTCTCTTTCGCGCCTGCTGGGCGCCCATCCAG	840
Qy	841	CTGTTCCTTGGTGTGTCAGGCGCTGGGCGCCCGCGGGCTTCCTGGCACCCAGCAGCTAGGCC	900	
Db	841	CTGTTCCTTGGTGTGTCAGGCGCTGGGCGCCCGCGGGTCTCTGGCACCCAGCAGCTAGGCC	900	
Qy	901	GCCTACGCGCTTAAGACTCGGGCTCACTGTCATGTCTTACAGCAACTCCGCGCTGAACCCG	960	
Db	901	GCCTACGCGCTTAAGACTCGGGCTCACTGTCATGTCTTACAGCAACTCCGCGCTGAACCCG	960	
Qy	961	CTGCTCTACGCTTCTCTGGGCTTCCGACAGGCTTCGCGCGGCTTCGCGCGGCTGCTGCCCTGC	1020	
Db	961	CTGCTCTACGCTTCTCTGGGCTTCCGACAGGCTTCGCGCGGCTTCGCGCGGCTGCTGCCCTGC	1020	
Qy	1021	CGCGCGCGCGCGCCCGCCCGCGCGCGGCTCCGACAGGCTTCGCGACCCCGCAGCCCCACAC	1080	
Db	1021	CGCGCGCGCGCGCCCGCCCGCGCGGCTCCGACAGGCTTCGCGACCCCGCAGCCCCACAC	1080	
Qy	1081	CGCGAGCTGCACCGCTTGGGCTCCACCCCGCGCCCGCCAGGGCGCAGAGCCAGGGAGC	1140	
Db	1081	CGCGAGCTGTCTCGCTTGGGCTCCACCCCGCGCCCGCCAGGGCGCAGAGCCAGGGAGC	1140	
Qy	1141	AGTGGGCTGCGCGCGCGCGGCTGTGGCTCTTGGGGAGGACAAACGCCCCCTCTCTGA	1197	
Db	1141	AGTGGGCTGCGCGCGCGCGGCTGTGGCTCTTGGGGAGGACAAACGCCCCCTCTCTGA	1197	
RESULT 14				
ADG19756				
ID	ADG19756	standard; cDNA; 1197 BP.		
XX	AC	ADG19756;		
XX	AC			
DT	26-FEB-2004	(first entry)		
DE		G protein coupled receptor (GPCR) 52872 coding sequence.		
XX		cytostatic; nephrotropic; antiinflammatory; cardiant; respiratory;		
KW		gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;		
KW		18636; 2466; 43238; 1983; 52881; 2398; 45449; 50289; 52872; 26908;		
KW		cellular proliferative disorder; brain disorder; renal disorder;		
KW		kidney disorder; inflammatory disorder; cardiovascular disorder;		
KW		liver disorder; intestinal disorder; respiratory disorder;		
XX		angiogenic disorder; human; G protein coupled receptor; GPCR; gene; ss.		
OS		Homo sapiens.		
XX				
FN		US2003215860-A1.		
XX				
PD		20-NOV-2003.		
XX				
FF		03-APR-2003; 2003US-00407079.		
XX				
PR		29-FEB-2000; 2000US-0186059P.		
PR		24-MAR-2000; 2000US-0191845P.		
PR		22-MAY-2000; 2000US-0206019P.		
PR		17-NOV-2000; 2000US-00715790.		
PR		28-FEB-2001; 2001US-007196338.		
PR		22-MAY-2001; 2001US-00863200.		
PR		22-AUG-2001; 2001US-0314041P.		
PR		22-AUG-2001; 2001US-0314185P.		
PR		21-AUG-2002; 2002US-00225094.		
PR		22-AUG-2002; 2002US-00226102.		
PR		15-OCT-2002; 2002US-00272417.		
PR		29-OCT-2002; 2002US-00282837.		
XX				
PA		(MILL-) MILLENNIUM PHARM INC.		
XX				
FI		Gluckemann MA, Silos-Santiago I, Carroll JM, Galvin KM;		
XX				
DR		WPI; 2004-010777/01.		
DR		P-PSDB: ADG19755.		

XX	PT	New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
XX	PT	45449, 50289, 52872 or 26908, useful in preparing a composition for
XX	PT	treating e.g., cellular proliferative, brain, kidney, inflammatory or
XX	PT	angiogenic disorder.
XX	Claim 1;	SEQ ID NO 94; 163pp; English.
XX	CC	The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
XX	CC	2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
XX	CC	sequence comprising 939-1489 bp or its fragment comprising at least 15
XX	CC	nucleotides; a sequence encoding a polypeptide comprising a sequence
XX	CC	having 223-852 amino acids, or its allelic variant or fragment comprising
XX	CC	at least 15 contiguous amino acids; or a sequence that hybridises with
XX	CC	(1) under stringent conditions. The nucleic acid or polypeptide is useful
XX	CC	in preparing a composition for treating a disorder characterised by
XX	CC	aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
XX	CC	26908 activity e.g., cellular proliferative, brain, renal, kidney,
XX	CC	inflammatory, cardiovascular, liver, intestinal, respiratory or
XX	CC	angiogenic disorder. This sequence encodes novel human protein 52872, a G
XX	CC	protein coupled receptor (GPCR).
XX	Seq	Sequence 1197 BP; 130 A; 481 C; 386 G; 200 T; 0 U; 0 Other;
XX	Query Match	99.9%; Score 1195.4; DB 12; Length 1197;
XX	Best Local Similarity	99.9%; Pred. No. 3.7e-167;
XX	Matches 1196;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1	ATGCACACGCTGGCTACGTCGGGACCCAAACGCGTCTCTGGGGGGACCGCGCAACGCGCTCC 60
Db	1	ATGCACACCGTGGCTACGTCGGGGCCCAACACGCGCTCTGGGGGGACCGCGCAACGCGCTCC 60
Qy	61	GGCTGCCCGGGCTGTGGGCGCCAAACGCTTCGGACGGGCCAGTCCCTTCGCGCGGGCGCGT 120
Db	61	GGCTGCCCGGGCTGTGGGCGCCAAACGCTTCGGACGGGCCAGTCCCTTCGCGCGGGCGCGT 120
Qy	121	GACGCTGGCTCTGTCCGCGCTCTTCTTCGCGCGCGTGTGCTGGGCGCTGTGGGGGAAC 180
Db	121	GACGCGTGGCTGTGGCGCTCTTCTTCGCGCGCGTGTGCTGGGCGCTGTGGGGGAAC 180
Qy	181	TGCGTGGTCACTAGTCACTTCGCGGCACAAAGCGGATGGGACCGTGCACCACTTCTAC 240
Db	181	TGCGTGGTCACTAGTCACTTCGCGGCACAAAGCGGATGGGACCGTGCACCACTTCTAC 240
Qy	241	ATGCCCAACTCGGCGGCCACGACGTGACCTTCTCTCTGTGCTGCGTCCCTTTCACGGCC 300
Db	241	ATGCCCAACTCGGCGGCCACGACGTGACCTTCTCTCTGTGCTGCGTCCCTTTCACGGCC 300
Qy	301	CTGCTGTACCCGCTCCCGGGCTGGGTGCTGGGCGCACTTCATGTGCAAGTTGTCACATAC 360
Db	301	CTGCTGTACCCGCTCCCGGGCTGGGTGCTGGGCGCACTTCATGTGCAAGTTGTCACATAC 360
Qy	361	ATCCACAGGTCTCGGTGACGGCCACGTGTGCGCACTCTGACCGGCATAGTGTGACCCGC 420
Db	361	ATCCACAGGTCTCGGTGACGGCCACGTGTGCGCACTCTGACCGGCATAGTGTGACCCGC 420
Qy	421	TGCTAGCTACCGGTGTCCTCCGTTGGCGCCCTGTCACCGCGCGCACGCCCGCGCTGGCGT 480
Db	421	TGCTAGCTAGCGGTGTCCTCCGTTGGCGCGCCCTGTCACCGCGCGCACGCCCGCGCTGGCGT 480
Qy	481	GCTGTGAGCCTCAGCATCTGGGTAGGGCTCTGCGCGGTGTCTGCGCGGTGCTCGGCCCTG 540
Db	481	GCTGTGAGCCTCAGCATCTGGGTAGGGCTCTGCGCGGTGTCTGCGCGGTGCTCGGCCCTG 540
Qy	541	CACCGCTGTACACCGGGCGCGCGCTTACCTGCAAGTGTGAGGCGCTTCCCGCGCGCCCTG 600
Db	541	CACCGCTGTACACCGGGCGCGCGCTTACCTGCAAGTGTGAGGCGCTTCCCGCGCGCCCTG 600
Qy	601	GACGCGGCTCTCGCACTGTACAACTCTGTCGGCGCTGTACTGCTGCGCGCTGCTGCGCAC 660
Db	601	GACGCGGCTCTCGCACTGTACAACTCTGTCGGCGCTGTACTGCTGCGCGCTGCTGCGCAC 660
Qy	661	TGCGCTGTATTCGCGCCATGCTGCGGCACCTGGGCGGGGTGCGCGTGTGCGCCCGCGCC 720

DR WPI; 2004-692829/68.
XX P-PSDB; ADS88807.
PT New GPR54 receptor agonists or antagonists, useful for treating
PT gonadotropin related disorders, e.g. hypogonadotropic hypogonadism, or
XX gonadotropin-estradiol/testosterone-dependent related cancers.
PS Disclosure; SEQ ID NO 1; 22pp; English.
XX
CC The specification describes an agonist or antagonist of the GPR54
CC receptor. This agonist or antagonist is used for treating a gonadotropin
CC related disorder. The GPR54 receptor agonist or antagonist is useful for
CC treating a gonadotropin related disorder, such as hypogonadotropic
CC hypogonadism, luteinising hormone (LH) and/or follicle stimulating
CC hormone (FSH) related disorders, or gonadotropin-estradiol/testosterone-
CC dependent related cancers. The present sequence encodes a human GPR54
CC receptor, which is used to identify agonists and antagonists of the
XX invention.
SQ Sequence 1197 BP; 130 A; 481 C; 385 G; 201 T; 0 U; 0 Other;
Query Match 99.9%; Score 1195.4; DB 13; Length 1197;
Best Local Similarity 99.9%; Pred. No. 3.7e-167;
Matches 1196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCACACCGTGGCTACGTCCGGACCCCAACCGCTCTCTGGGGGGCACCGCCCAACGCTCC 60
Db 1 ATGCACACCGTGGCTACGTCCGGACCCCAACCGCTCTCTGGGGGGCACCGCCCAACGCTCC 60
QY 61 GGTCTCCCGGGTGTGGGGCCCAACCGCTCTGGACCGCCCAAGTCTCTTCCGCGGGCCGTG 120
Db 61 GGTCTCCCGGGTGTGGGGCCCAACCGCTCTGGACCGCCCAAGTCTCTTCCGCGGGCCGTG 120
QY 121 GACGCTGGCTGTGCGCGCTCTTCTTCCGGCGCTGATGCTCTGGGGCTGTGGGGGAC 180
Db 121 GACGCTGGCTGTGCGCGCTCTTCTTCCGGCGCTGATGCTCTGGGGCTGTGGGGGAC 180
QY 181 TCGCTGGTCACTACGTATCTGCGCCACAAAGCCGATGCGGACCGGTGACCAACTTCTAC 240
Db 181 TCGCTGGTCACTACGTATCTGCGCCACAAAGCCGATGCGGACCGGTGACCAACTTCTAC 240
QY 241 ATGCGCAACCTGGCGGGCCACGAGCGTTCCTCTCTGCTGTGCTGCTCCCTTCAACGCC 300
Db 241 ATGCGCAACCTGGCGGGCCACGAGCGTTCCTCTCTGCTGTGCTGCTCCCTTCAACGCC 300
QY 301 CTGCTGTACCCGCTGCGCGGCTGGGTGTGCGCGGCTTCAATGTGCAAGTTCGTCAACTAC 360
Db 301 CTGCTGTACCCGCTGCGCGGCTGGGTGTGCGCGGCTTCAATGTGCAAGTTCGTCAACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGAGGCCACGCTGTGCGACCTCTGACCGCCATGAGTGTGGACCGC 420
Db 361 ATCCAGCAGGTCTCGGTGAGGCCACGCTGTGCGACCTCTGACCGCCATGAGTGTGGACCGC 420
QY 421 TGGTACGTGACGCTGTCCGCTTGGCGGCTTGCACCGCGCAACCGCGGCTGTGCGCTG 480
Db 421 TGGTACGTGACGCTGTCCGCTTGGCGGCTTGCACCGCGCAACCGCGGCTGTGCGCTG 480
QY 481 GTGTGACGCTGACGCTGTGGGTAGGCTGTGGGGGCTGTCTGCGCGGCTGTGCGCGCTG 540
Db 481 GTGTGACGCTGACGCTGTGGGTAGGCTGTGGGGGCTGTCTGCGCGGCTGTGCGCGCTG 540
QY 541 CACCGCGCTGTACCCGCGGCGCGGCTTACTGACGTGAGGCGCTTCCCGACGCGCGCCCTG 600
Db 541 CACCGCGCTGTACCCGCGGCGCGGCTTACTGACGTGAGGCGCTTCCCGACGCGCGCCCTG 600
QY 601 GAGCGCGCTTCCGCACTGTACAACTGTCTGGCGCTGTACCTGTCTGCTGCTGCTGCTG 660
Db 601 GAGCGCGCTTCCGCACTGTACAACTGTCTGGCGCTGTACCTGTCTGCTGCTGCTGCTG 660
QY 661 TCGCGCTGTATGCGGCGCATGTGCGCGCACTGTGGCGCGGCTGCGCGTGGCGCGCGCC 720
Db 661 TCGCGCTGTATGCGGCGCATGTGCGCGCACTGTGGCGCGGCTGCGCGTGGCGCGCGCC 720

QY 721 GCCGATAGCGCCCTGACAGGGCAGGTGCTGGCAGAGCGCGAGCGCGCTGTGGGCGCCAAAG 780
Db 721 GCCGATAGCGCCCTGACAGGGCAGGTGCTGGCAGAGCGCGAGCGCGCTGTGGGCGCCAAAG 780
QY 781 GTCTCGCGGCTGTGGCGGCGCTGTCTGTCTTTCGGCGGCTGTGTGGGCGGCGCTGTCCAG 840
Db 781 GTCTCGCGGCTGTGGCGGCGCTGTCTGTCTTTCGGCGGCTGTGTGGGCGGCGCTGTCCAG 840
QY 841 CTGTTCTCTGTGTGCTGACGGCGCTGGGCGCCCGCGGCTCTTGGSCACCCACGACGCTACGCC 900
Db 841 CTGTTCTCTGTGTGCTGACGGCGCTGGGCGCCCGCGGCTCTTGGSCACCCACGACGCTACGCC 900
QY 901 GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTTACAGCAACTCCGCGCTGAACCGG 960
Db 901 GCCTACGCGCTTAAGACCTGGGCTCACTGCAATGCTTACAGCAACTCCGCGCTGAACCGG 960
QY 961 CTGCTCTACGCGCTTCTTGGGCTTGGGCTTCCGACAGGCGCTTCCGCGGCTGTGCGCGCTGC 1020
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Search completed: February 15, 2006, 02:17:25
Job time : 813 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 02:04:01 ; Search time 6317 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 5893141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 3: gb_env.*
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- 10: gb_sts.*
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- 13: gb_vi.*
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- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1197	100.0	1197	6	CS081629 Sequence
2	1197	100.0	1197	6	E44032 Novel G pro
3	1197	100.0	1197	6	AR481881 Sequence
4	1197	100.0	1197	6	AX549191 Sequence
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6	1197	100.0	1197	8	AY029541 Homo sapi
7	1197	100.0	1197	8	AY253981 Homo sapi
8	1197	100.0	1450	6	CQ324743 Sequence
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10	1195.4	99.9	1197	6	BD269602 G protein
11	1195.4	99.9	1197	6	CQ878955 Sequence
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14	1195.4	99.9	1197	8	HS430820 Homo sapi
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DEFINITION	CS081629	CS081629.1	GI:66348928			
ACCESSION	CS081629					
VERSION	CS081629.1					
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ORGANISM	Homo sapiens					
REFERENCE	1	Yamamoto, N., Matsumoto, H., Hayashi, F. and Tajimi, M.				
AUTHORS		Regulation of human metacilin recognising receptors				
TITLE		Patent: WO 2005040833-A 1 06-MAY-2005;				
JOURNAL		Bayer HealthCare AG (DE)				
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LOCUS Novel G protein-coupled receptor protein and DNA and ligand of the
DEFINITION same
ACCESSION E44032
VERSION E44032.1 GI:18621998
KEYWORDS JP 2000312590-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1197)
AUTHORS Watanabe,T., Terao,S., Araya,Y., Otaki,T., Kanehas,K. and Kitada,C.
TITLE Novel G protein-coupled receptor protein and DNA and ligand of the
JOURNAL Patent: JP 2000312590-A 4 14-NOV-2000;
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COMMENT OS Homo sapiens (human)
PN JP 2000312590-A/4
PF 14-NOV-2000
PR 29-SEP-1999 JP 1999276225
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KIMINO KANEHASHI,
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Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION AR481881
VERSION AR481881.1 GI:47243624
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SOURCE Unknown.
ORGANISM Unknown.

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Watanabe T., Terao Y., Shintani Y., Ohtaki T., Kanehashi K. and
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Peptides that activate the G-protein coupled receptor protein,
07/71175
Patent: US 6699965-A 6 02-MAR-2004;
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ACCESSION AX549191
VERSION AX549191.1 GI:25813906
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Hominidae; Homo.
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REFERENCE Burmer,G.C., Roush,C.L. and Brown,J.P.
AUTHORS Antigenic peptides, such as for G protein-coupled receptors
TITLE (GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 476 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.7e-114;
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LOCUS Homo sapiens hot71t175 mRNA for G protein-coupled receptor, complete
DEFINITION cda.
ACCESSION AB051065
VERSION AB051065.1 GI:14041797
KEYWORDS

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ORGANISM    Homo sapiens
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Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS    Ohtaki,T., Shintani,Y., Honda,S., Matsumoto,H., Hori,A.,
            Kanehashi,K., Terao,Y., Kumano,S., Takatsu,Y., Masuda,Y.,
            Ishibashi,Y., Watanabe,T., Asada,M., Yamada,T., Suenaga,M.,
            Kitada,C., Usuki,S., Kurokawa,T., Onda,H., Nishimura,O. and
            Fujino,M.
TITLE      Metastasis suppressor gene KiSS-1 encodes peptide ligand of a
            G-protein-coupled receptor
JOURNAL    Nature 411 (6837), 613-617 (2001)
PUBMED     11385580
REFERENCE   2 (bases 1 to 1197)
AUTHORS    Shintani,Y., Terao,Y. and Watanabe,T.
TITLE      Direct Submission
JOURNAL    Submitted (12-NOV-2000) Yasushi Shintani, Takeda Chemical
            Industries, Ltd., Pharmaceutical Discovery Research Division; 10
            Wadai, Ysukuba, Ibaraki 300-4293, Japan
            (E-mail:Shintani.Yasushi@takeda.co.jp, Tel:81-298-64-5011,
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DEFINITION Homo sapiens putative G protein-coupled receptor mRNA, complete cds.
ACCESSION AY029541
VERSION   AY029541.1 GI:15626067
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REFERENCE 1 (bases 1 to 1197)
AUTHORS   Kotani,M., Detheux,M., Vandenbogaerde,A., Communi,D.,

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Vanderwinden,J.M., Le Poul,E., Brezillon,S., Tyldesley,R.,
Suarez-Huerta,N., Vandeput,F., Bianpain,C., Schiffman,S.N.,
Vassart,G. and Parmentier,M.
The metastasis suppressor gene KISS-1 encodes kisseptins, the
natural ligands of the orphan G protein-coupled receptor GPR54
J. Biol. Chem. 276 (37), 34631-34636 (2001)
11457843
2 (bases 1 to 1197)
Kotani,M., Decheux,M. and Parmentier,M.
Direct Submission
Submitted (10-APR-2001) IRIHBN, Universite Libre de Bruxelles, 808,
Route de Lennik, Brussels B-1070, Belgium
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DEFINITION Homo sapiens hypogonadotropin-1 (GPR54) mRNA, complete cds.
ACCESSION AY253981
VERSION AY253981.1 GI:32454259
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ORGANISM Homo sapiens
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Clausenhardt,S.A., Guseilla,J.F., O'Rahilly,S., Carlton,M.B.,
Crowley,W.F. Jr., Aparicio,S.A. and Colledge,W.H.
The GPR54 gene as a regulator of puberty
N. Engl. J. Med. 349 (17), 1614-1627 (2003)
14573733
2 (bases 1 to 1197)
Seminara,S.B., Acierno,J.S. Jr., Shagoury,J.K., Bo-Abbas,Y.,
Kuchung,W., Kaiser,U.B., Slangenaupt,S.A., Guseilla,J.F. and
Crowley,W.F. Jr.
Mutations in a G Protein-coupled Receptor, GPR54, Cause Autosomal
Recessive Idiopathic Hypogonadotropic Hypogonadism

JOURNAL Unpublished (2003)
REFERENCE 3 (bases 1 to 1197)
AUTHORS Seminara,S.B., Acierno,J.S. Jr., Shagoury,J.K., Bo-Abbas Y., Kuohung,W., Kaiser,U.B., Slaughaupt,S.A., Gubella,J.F. and Crowley,W.F. Jr.
TITLE Direct Submision
JOURNAL Submitted (10-MAR-2003) Reproductive Endocrine Unit, Massachusetts General Hospital, Bartlett Hall Extension, Room 505, 55 Fruit Street, Boston, MA 02114, USA
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ACCESSION CQ924743
VERSION CQ924743.1 GI:56214300
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Follettie,M.T.
TITLE Methods utilising g-protein coupled receptor 54
JOURNAL Patent: WO 2004098855-A 1 11-NOV-2004;
WYETH (US)
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genes encoding them, and their production and use.					
ACCESSION					
BD095775					
VERSION					
BD095775.1 GI:22641363					
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WO 0148189-A/33.					
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Homo sapiens (human)					
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Suwa,M. and Sugiyama,T.					
Novel guanosine triphosphate-bound protein-coupled receptors and					
genes encoding them, and their production and use					
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HELIX RESEARCH INSTITUTE,SHUNICHIRO MATSUMOTO,TAMAKI ODA,YOKO					
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MORIKAWA,KENJI YOSHIDA,					
PI MAKIKO SUWA,TOMOYASU SUGIYAMA					
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DEFINITION Sequence 1 from Patent WO2004087622.
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VERSION CQ891716.1 GI:55164312
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Hominoidea; Homo.
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de Roux,N., Genin,E., Milgrom,E., Chausseain,J.L. and Carel,J.C.
Gpr54 receptor agonist and antagonist useful for the treatment of
gonadotropin related diseases
Patent: WO 2004087622-A 1 14-OCT-2004;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR); UNIVERSITE RENE DESCARTES (PARIS V) (FR); UNIVERSITE
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ORIGIN

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VERSION AX239652.1 GI:15797325
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Hominoidea; Homo.
REFERENCE 1
AUTHORS Glucksmann, M.A., Galvin, K.M. and Silos-Santiago, I.
TITLE 1983, 52881, 2398, 45449, 50289, and 52872, G protein-coupled
receptors and uses therefor
JOURNAL Patent: WO 0164882-A 18 07-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Hominoidea; Homo.
REFERENCE 1
AUTHORS Muir, A.I., Chamberlain, L., Elshourbagy, N.A., Michalovich, D.,
Moore, D.J., Calamari, A., Szekeres, P.G., Sarau, H.M., Chambers, J.K.,
Murdoch, P., Steplewski, K., Shabon, U., Miller, J.E., Middleton, S.E.,
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Darker, J.G., Larminie, C.G., Wilson, S., Bergsma, D.J., Emson, P., Faull, R., Philpott, K.L. and Harrison, D.C.
AXOR12, a novel human G protein-coupled receptor, activated by the peptide KiSS-1
J. Biol. Chem. 276 (31), 28969-28975 (2001)

ORIGIN

[illegible][illegible]

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-771-417-6

Perfect score: 1197

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Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

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6: /cgn2_6/prodata/1/pubpna/us10_NEW_PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/us10_NEW_PUB.seq1:*
8: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq:*
9: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq2:*
10: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq3:*
11: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq4:*
12: /cgn2_6/prodata/1/pubpna/us60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	81.0	67.7	1188	11	US-11-136-527-2760
2	378.8	31.6	600	11	US-11-136-527-6856
3	148.2	12.4	3985	11	US-11-136-527-3404
4	146.2	12.2	1290	11	US-11-136-527-2457
5	146.2	12.2	1290	11	US-11-136-527-6553
6	145.2	12.1	1163	11	US-11-136-527-2458
7	139.4	11.6	1238	7	US-10-995-561-321
8	139.4	11.6	1498	7	US-10-995-561-320
9	139.4	11.6	86131	7	US-10-995-561-13298
10	134.6	11.2	2327	11	US-11-136-527-3190
11	110.2	9.2	1685	7	US-10-750-185-36071
12	110.2	9.2	1685	7	US-10-750-623-36071
13	108.4	9.1	1293	6	US-10-508-892-1
14	108.4	9.1	1293	7	US-10-992-577-7
15	107.4	9.0	1350	11	US-11-136-527-463
16	107.4	9.0	3129	11	US-11-136-527-3314
17	105.8	8.8	1423	11	US-11-136-527-2066
18	99.4	8.3	6244	11	US-11-136-527-3243
19	98.6	8.2	3635	11	US-11-136-527-2101
20	97.8	8.2	79528	7	US-10-276-233A-6
21	94.8	7.9	1584	11	US-11-136-527-2136

22	94	7.9	1410	7	US-10-992-577-1	Sequence 1, Appli
23	90	7.5	1523	11	US-11-127-877-30	Sequence 30, Appl
24	90	7.5	2955	11	US-11-136-527-2954	Sequence 2954, Ap
25	89.4	7.5	2471	11	US-11-136-527-2231	Sequence 2231, Ap
c	86.4	7.2	1224	7	US-10-750-185-40492	Sequence 40492, A
c	86.4	7.2	1224	7	US-10-750-623-40492	Sequence 40492, A
28	85	7.1	1384	11	US-11-136-527-2159	Sequence 2159, Ap
29	83.6	7.0	1400	11	US-11-136-527-7225	Sequence 7225, Ap
30	83.6	7.0	1769	11	US-11-136-527-3129	Sequence 3129, Ap
31	83	6.9	1560	11	US-11-136-527-3742	Sequence 3742, Ap
32	83	6.9	1865	7	US-10-533-355-9	Sequence 9, Appli
33	82.2	6.9	1452	11	US-11-136-527-3122	Sequence 3122, Ap
34	82.2	6.9	2116	11	US-11-136-527-3819	Sequence 3819, Ap
35	79.8	6.7	1524	11	US-11-136-527-3421	Sequence 3421, Ap
36	78.8	6.6	4357	6	US-10-513-118-1	Sequence 1, Appli
37	78.2	6.5	3883	11	US-11-136-527-3673	Sequence 3673, Ap
38	78.2	6.5	4963	11	US-11-136-527-3442	Sequence 3442, Ap
39	77	6.4	1376	7	US-10-502-893-1	Sequence 1, Appli
40	76.8	6.4	1376	7	US-10-627-633-3	Sequence 3, Appli
41	76.2	6.4	600	11	US-11-136-527-6554	Sequence 6554, Ap
42	76.2	6.4	11070	11	US-11-075-185-34	Sequence 34, Appli
43	76.2	6.4	78869	11	US-11-075-185-1	Sequence 1, Appli
44	75.4	6.3	10968	11	US-11-075-185-35	Sequence 35, Appli
45	75.2	6.3	2162	11	US-11-127-877-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-11-136-527-2760

; Sequence 2760, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2760

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-2760

Query Match	67.7%	Score 810;	DB 11;	Length 1188;
Best Local Similarity	82.3%	Pred. No. 6.5e-114;		
Matches 953;	Conservative 1;	Mismatches 201;	Indels 3;	Gaps 2;
QY	1	ATGCACACCGTGGCTACGTCGGAGCCCAACCGGCTCTCGGGGGGCACCGGCCAACGCTTCC	60	
Db	1	ATGGCCGCGAGAGGCGACGTTGGTCCGAACTGGTGGCTCGTCCACGCTTCCG	60	
QY	61	GGCTCCCGGGCTGTGGGCGCAACCGCTCGAGCGGCCAGTCCCTTCGCGCGGGCGGTG	120	
Db	61	GGATCCCGGGCTGCGGTGTCAATCCCTCGATGGCCAGGCTCGCGCGAGGCCCCCTG	120	
QY	121	GACGCTGGCTGTCGCGCTCTTCTTCGCGGGCTGTGCTGCTGGGCTGTGTGGGGAAC	180	
Db	121	GATGCTGGCTGGTGGCTGGCTGTTCCTGCTCCCTTAATGTTGCTGGGGCTAGTCGGGAAC	180	
QY	181	TGCTGGTTCATCTAGCTCATCTGCGCCCAACGCGATCGGACCGCTGACCAACTTCTAC	240	
Db	181	TCATGGTTCATCTGTTATCTGCGCCCAACGACATGACGACCGTCCACCAATTTCTAC	240	
QY	241	ATGCGCAACCTGGGCGCCACGAGCTGACCTTCCTTCCTGTGTGCTGCTCCCTTCACGGCC	300	
Db	241	ATCGCTAACCTGGGCGCCACAGATGTCCTTCTTCTTCTGCTGCTGCTACCTTCACCGCG	300	

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QY 301 CTGCTGTACCGCTGCCCGCTGGGTGCTGGCGACCTTCATGTGCAAGTTCTGTCACACTAC 360
Db 301 CTCCTCTATCCGCTGCCACCTGGGTGCTGGAGACTTCATGTGCAAAATTCGTCAACTAC 360
QY 361 ATCCAGCAGGTCTCGGTGAGGCCACGTGTGCACCTCTGACCGCATAGTGTGACCGC 420
Db 361 ATCCAGCAGGTCTCGGTGAGGCCACATGTGCCACTTTGACAGCCATAGTGTGACCGC 420
QY 421 TGGTACGTACAGGTGTTCCGCTGCGCGCCCTTGCAACCGCCGACGCCGCCCTGCGGTG 480
Db 421 TGGTACGTACGTGTTCCGCTGCGCGCCCTTACACCGCGACCTTCACCGCGCTGCGCCCTG 480
QY 481 GCTGTACGCTCAGCATCTGGTAGGCTCTGGGGGGGTGTCTGGCGGGGTGCTGCGCCCTG 540
Db 481 ACTGTACGCTTAGCATCTGGGTGGGTTCGCGAGCTGTTCCGCGCCCGGTGCTGAGCTCTG 540
QY 541 CACCGCTGTACACCGGGCGCGCGCTACTGCACTGAGGCTTCCCGCAGCGCGCGCTG 600
Db 541 CACCGCTGTGCGCGCGCGCTCACACCTACTGCACTGAGGCTTTCACGAGCGGTGCGCTG 600
QY 601 GAGCGCGCTTTCGCACTGTACAACTGCTGGCGCTGTACCTGCTGCGCTGCTGCGCCACC 660
Db 601 GAGCGCGCTTTCGCGCTGTACAACTGCTGGCGCTGTACCTGCTGCGCTGCTGCGCCACC 660
QY 661 TCGCGCTGCTATCGCGCCATGCTGCGCACCTGCGCGGGGTGCGCGTGGCGCGCGCGCC 720
Db 661 TCGCGCTGCTATCGGTGCCATGCTGCGCACCTGCGCGGGGTGCGCGTGTACGCGCGCGACC 720
QY 721 GCGGATAGCGCTTCAGGGGCGAGTGTGGCAGAGCGCAGCGCGCGCGCTGCGGGCCAAAG 780
Db 721 ACTGATGGCGCTTCAGGGGCGAGTGTGTAGCAGCGCGCTGAGCAGTGTGCGCACCAAG 780
QY 781 GTCTCGCGCTGTGTGGCGCGTGTCTCTGCTCTTCGCGCGCTGCTGGGGGCCCATCCAG 840
Db 781 GTCTCGCGCTGTGTGGCGCTGTCTCTGCTCTTCGCGCGCTGCTGGGGGCCCATCCAG 840
QY 841 CTGTTCTCTGGTCTCAGCGCGTGGCGCGCGCGCGCGCTCTGCGCACCGCAGCTACGCC 900
Db 841 CTGTTCTCTGGTCTTCAAGCCCT--GCCGCTCGGGGGCTTGGCACCCCTCGAAGCTATG-C 897
QY 901 GCTACGCGCTTAAAGCTTGGGCTCACTGCACTGTCTTTCGCGCGCTGCTGGGGGCCCATCCG 960
Db 898 GCCTACGCGCTCAAGATCTGGGCTCACCTGCACTGTCTTACAGCAATTCCTGCGCTCAACCCG 957
QY 961 CTGCTCTACGCTTCTCGGCTCGCATCTTCGACAGGCTTTCGCGCGGTCTGCGCCCTGC 1020
Db 958 CTGCTCTATGCTTCTCGGTTCCCACTTCAGACAGGCTTCTGCGCGGTGTGCGCCCTGC 1017
QY 1021 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1080
Db 1018 GCGCGCGCAACGCGCAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 1077
QY 1081 GCGGAGCTGACCGCTGCGGTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGC 1140
Db 1078 AGTGTGCGCACAGCGCGGCTGCGCACCTGTCTCGGCTCAGAACCCCGCGCGCGCGGAAAC 1137
QY 1141 AGTGGGCTGGCGCGCGC 1158
Db 1138 CCGTGTGGTGCCTCGCC 1155
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RESULT 2

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US-11-136-527-6856
; Sequence 6856, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
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; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6856
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6856
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Query Match 31.6%; Score 378.8; DB 11; Length 600;
Best Local Similarity 81.2%; Pred. No. 4.1e-49;
Matches 463; Conservative 1; Mismatches 103; Indels 3; Gaps 2;

QY 589 AGCCGCGCCCTGAGCGCGCTTCGCACTGTGTACAACTGTGTGGCGGTGTACTGTGCGG 648
Db 1 AGCCGTCCTTGGAGCGCGCTTCGCGCTCTACAACTGTGTGGCGGTGTACTGTGCGGCGG 60
QY 649 CTGCTCGCCACCTGCGCGCTGCTATGCGGCATGTGTGGCCACCTTGGGCGGGTTCGCGGTG 708
Db 61 CTGCTCGCCACCTGCGCGCTGCTACGCTGTGCTGCGCCACCTTGGGCGCGCGCGCTGTA 120
QY 709 CGCCCGCGCGCGCGCGATAGCGCGCTGAGGGGCGAGGTGTGTGGCAGAGCGCGCAGGCGCC 768
Db 121 CGCCCGCGCACCCACTGATGGCGCGCTGAGGGGCGAGGTGTGTAGCAGAGCGCGCTGAGCA 180
QY 769 GTGCGGGCCAAAGTCTCGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
Db 181 GTGCGCACCAAGTCTCGCGCGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 829 GGCCCGCATCCAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
Db 241 GGCCCGCATCCAGCTGCTTCTGCTGCTTCAAGCCCT--GCCGCTCGGGGGCTTGGACCCCT 298
QY 889 CGCAGCTACGCGCGCTACGCGCTTAAAGCTTGGGCTCACTGCACTGTCTCTACAGCAACTCC 948
Db 299 CGAAGCTATGC-GCTACGCGCTCAAGATCTGGGCTCACTGCACTGTCTCTACAGCAATCT 357
QY 949 GCGTGAACCGCGTCTCTACGCTTCTGCGGTTCGCACTTTCGACAGGCTTTCGCGCGC 1008
Db 358 GCGTCAACCGCGTCTCTATGCTTCTGCGGTTCGCACTTTCGACAGGCTTTCGCGCGC 417
QY 1009 GTCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1068
Db 418 GTGTGCGCGCTGCGCGCGCGCAACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAG 477
QY 1069 GCAGCGCCACACGCGGAGCTGCAACGCTGCGGTTCGCAACCGCGCGCGCGCGCGCGCGCGCAG 1128
Db 478 GCGCACCCCATAGTGTGCGCGCACGCGGGCTGCGCACCTGTCTCGGGTTCAGGACCCCGC 537
QY 1129 AAGCCAGGAGCATGTGGCTGCGCGCGCGC 1158
Db 538 GAGCCTGGGAACCTGTGTGCTGCTCGCC 567
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RESULT 3

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US-11-136-527-3404
; Sequence 3404, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3404
; LENGTH: 3985
; TYPE: DNA
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; ORGANISM: Rattus norvegicus
US-11-136-527-3404

Query Match      12.4%; Score 148.2; DB 11; Length 3985;
Best Local Similarity 51.5%; Pred. No. 1.6e-14; Indels 20; Gaps 6;
Matches 497; Conservative 0; Mismatches 448;

QY 82 AACGCTCGAGACGGCCAGTCCCTTCGCGCGCGCGCGTGGAGCGCTCGGTGCGCGCTC 141
DB 746 AATGCACTGCTGGCACTAGCCTGGCAGGACTGGCTGTGAGTGCATCTTGATCTCTCTG 805
QY 142 TTCTTCGCGCGCTGATGCTGTGCGCTGTGGGAACTCGCTGTGTCATCTACGTCATC 201
DB 806 GTGTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 865
QY 202 TGGCGGCAAGCCGATGGGACCGTGACCACTTCTATCGCCCACTCGCCGCGGCGCAG 261
DB 866 CTGCGGCACAGCTCAGCCCATCAGTGACAGTGCTATATCTCAACCTGGGACTGGCT 925
QY 262 GAGTGACCTTCCTCCTGTGCTGCTCCGCTTCACGCGCGCTGTGTACCCGCTGCCCGGC 321
DB 926 GAGCAACTCTTCATGCTG---GGGCTACCTTTCTGGCTGCTCAGAACGCCCTGTCTTAC 982
QY 322 TGGGTGCTGGGCACTTCATGTGCAAGTTGTCACACTATCATCAGCAGGTCTCGGTGACG 381
DB 983 TGGCCCTTTCGGCTCTCTCATGTGTCTGTCTGTGTCATGGCCGTGGATGGCATCAACAGTTC 1042
QY 382 GCCACGTGTGCCACTCTGACCGCATGAGTGTGGACCGCTGTGTCAGTACGCTGTTCGCG 441
DB 1043 ACCAGCATCTTCGCTCTACCCGTCATGAGTGTGGACCGTCACTGTGCTGTGTCACCCC 1102
QY 442 TTGCGCGGCTGACACCGCGCAGCGCCGCTGGCGCTGGCTGCTCAGCTCAGCTCAGTCTG 501
DB 1103 ACAGCTCTGCCGCTGGGCGACGCGCACTGTGGCTCGAATGGTCACTGAGCTGTCTG 1162
QY 502 GTAGGCTCTGCGCGGTGTGTGCGCGGTGTGCGCCCTGCAACCGCTGTCAACCGCGCG 561
DB 1163 GTGGCTCTAGCTGTGGTGTGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1222
QY 562 CGGCGCTACTGCACTGAG--GCCCTCCACAGCGCGCCCTGGAGCG--GCCCTTCGCACTG 618
DB 1223 AGCAGCTGCCATGCACTGGCGAGCGCGGCTGCGCTGGCGAACAGCGCTTCATCATC 1282
QY 619 TACAACCTGTGCGCGTGTACCTGTGCTGCGCTGCTGCGCCACTGCGCCCTGTATGCGGC 678
DB 1283 TATACGCGCGCACTGGGCTTTTGTGGCCCTGCTGTGTATCTGTATGCTACCTGCTT 1342
QY 679 ATGCTCGCCACCTG--GGCGGGTTCGCTGCGCCCGCGCGCGCGGATAGCGCCCTGCA 737
DB 1343 ATTGTGTGAAGTGGGTGCGACCAACAGCGGGTGGCGCGCCCTCGTGCCAGTGGTA 1402
QY 738 GGGGAGAGTGTGGCAGAGGCGCAGCGCGGTGGCGGCAAGGTCTCGCGGCTGTGTGCG 797
DB 1403 CAGGCAACCGCTTGGCAGCGCGCGCGCTCTGAGCG--CAGGGTGACACGCACTGTGTGT 1461
QY 798 GCGCGTGTCTGCTCTTCTGCGCGCTGCTGGGCGCCCATCCAGCTGTCTCTGTGTGCA 857
DB 1462 GGTGTGTGTGGACTCTTGTCTCTGTGCTGGAATGCTTCTATTTACTCAACATCGTTAA 1521
QY 858 GCGGCTGGGCGCGCGGCTCTGTCGACCAACAGCAGCTACGCGCGCTACGCGCTTAAGAC 917
DB 1522 TGTGTGTGCGC-----GCTGCGGAGGAGCGGCTTCTTTGGGCTCTACTT 1569
QY 918 CTGGGCTCATGTCATGCTTACAGCACTTCGCGCTGAAACCGCGTGTCTTACGCTTCT 977
DB 1570 CTGTGTGTGTGCGCTGCTTACGCCAACAGCTGCGCAACCCCATCTCTACGGCTTCT 1629
QY 978 GGGCTCGCACTTCGACAGGCTTTCGCGCGCTGCTGCGCGCTGCGCGCGCGCGCGCG 1037
DB 1630 CTCCTACCGCTTCAAGCAGGGCTTCCGCGAGATCTGCTTAAGACCTTCTCGCGGATACG 1689
QY 1038 CGGCC 1042

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DB 1690 GAGCC 1694

RESULT 4
US-11-136-527-2457
; Sequence 2457, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2457
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2457

Query Match      12.2%; Score 146.2; DB 11; Length 1290;
Best Local Similarity 50.5%; Pred. No. 3.4e-14; Indels 45; Gaps 4;
Matches 497; Conservative 0; Mismatches 443;

QY 52 AACGCTCGGCTGCGCGGCTGTGGCGCAACGGCTCGGACGCGGCGGCTGCTGCGCG 111
DB 145 AATGCTCGGCGAGCGCGGCGCGAGAACACGAGCACGAAAGGCGGTAGCGCGCGCTG 204
QY 112 CGGCGCGTGGAGCCCTGGCTCGTGGCGCTCTTCTTGGCGCGCTGATGTGCTGGCGCTG 171
DB 205 CAGCCTGAGGCGGTC---CTGTACCCCTATTTTTCGGCGCTCATCTTCTCGTGGGCA 261
QY 172 GTGGGGAATCTCGCTGTCTATCTACCTGTCTCGCGCAACAGCGCATGCGGCGGCG 231
DB 262 GTGGGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 321
QY 232 AACTTCTATCGCAACCTGGCGGCAAGGAGTGAACCTTCTCTGTGTGTGTGTGTGTGT 291
DB 322 AACCTGTCTCATCTCAAGCTGGCGGCTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 381
QY 292 TTCAAGCGGCTGTCTACCGCTGCGCGCTGGGTGCTGGGCGACTTATGTGTGCAAGTTC 351
DB 382 TTCCAGGCGCACTACATACACCTTGAGCGACTGGGTGTTCGGCTGCTCTGTGCAAGGT 441
QY 352 GTCAACTATCATCCAGAGTCTCGGTGCGAGGCGACGTGTGCCACTCTTGACCGCATGAGT 411
DB 442 GTTCATTTCTCATCTTCTCACTATGACGCGCAGAGCTTACGCTGGCGCGCTCTCC 501
QY 412 GTGGACCGCTGTGTACGTACGCGTGTTCGCGTTGCGCGCGCTGCAACGCGCGCAACGCG 471
DB 502 CTGGACAGGTATCTGCCATCGCTACCGCTGCACTCCGAGAGTTGCGCACACCTCGA 561
QY 472 CTGGCGCTGGCTGTGTCAGCTCAGCATCTGGGTGAGGCTGTGGCGCGGTGTCTGGCGG 531
DB 562 AACCGCTGGCGCGCATCGGGCTCATCTGGGGGCTAGCACTGCTCTTCTTCGCGGCGCTAC 621
QY 532 CTGCGGCTGCAACCGCTGTCAACCGCGCGCGCGCTACTGCACTGAGGCGCTTCCCGACG 591
DB 622 CTGAGCTACTACCGTCTGAGTGGCGAGCTGGCCAACTGACAGTATGCCACCGAGATGGAG 681
QY 592 CGCGCGCTGGAGCGCGCTTTCGCACTGTACACCTGTCTGGCGCTGTACCTGTGTGGCG 651
DB 682 GCACCTCGAGCTCGAGCCATGGACCTCTGCACCTTCTGTCTTTAGCTACCTGTGTCCAG 741
QY 652 CTGCGCACTGGCGCTGTGTATGCGGCCATGTGCGGCCACTGGGCGGGTTCGCGGTGCG 711
DB 742 CTAGTCTCAGTCTGACCTATGCGGCTACCTGTGCGCTACCTGTGGCGCACAGTTCGAC 799
QY 712 CCGCGCGCGCGGATAGCGGCTCTGCGAGGGGCGAGGTGCTGGCAGAGCGCGCGCGCTG 771

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QY 174 GGGGAACTCGTGGTCACTACGTCACTCTGCGCCCAAGCCGATGCGGACCGTGACCAA 233
Db 139 GTTGGCTGTGCTACTGACGCTGGCCAAAGTGCCTGGCAGGAGCCAAAGSAGTACCAAGA 198
QY 234 CTTCTACATGCGCAACCTGGCGGCCACGAGCGTACCTTCTCTGCTGTGCTGCTGCCCTT 293
Db 199 TCTCTTCACTCCCACTTGGCGGTGGCCGACCTTTGCTTCACTCTGTGCTGCTGCCCTT 258
QY 294 CACGGCCCTGCTGTACCCGCTGCCGCTGGGCTGGGCGACTTCACTGCAAGTTGCT 353
Db 259 CAGGCGACCACTACACTGGATGCTTGGCTTCTTTGGGGCTTTCGTGTGCAAGCGGT 318
QY 354 CAATACATCCAGCAGGTCTCGGTGCAAGCCAGTGTGCCACTCTGACCGCATGAGTGT 413
Db 319 ACATCTGCTCATCTACCTCACCATGTATGCCAGCAGCTTCACTTGGCGGCTGTCCCT 378
QY 414 GGACCGCTGGTAGCTGACGGTGTTCCTGTTGGCGCCCTGCAACCGCGGCGCT 473
Db 379 GGACAGGTACCTGGCTGTGCGGACCMACCTGGCTTCCAGAGCCCTGCGCACCCCGGCAA 438
QY 474 GCGCTGGCTGTGAGCTCAGCATCTGGGTAGGCTCTGGCGGGTGTCTGCGCGGTGCT 533
Db 439 CGCGCGCGCGGTGGGCTGTGTGGCTGTGCTGGGGCTCTCTTTTCGCGGCCCTACCT 498
QY 534 CGCCCTGCAACCGCTGTCAACCGGCGCGCGCTACTGCAAGTGGCTTCCCGAGCG 593
Db 499 AAGCTAYTACGGCACGGTGGCTACGGCGGCTCGAGCTCTGCTGCGCGCTGGAGGA 558
QY 594 CGCCCTGGAGCGGCTTTCGCACTGTAAACCTGTGCGGCTGTACTGCTGCGCGTGT 653
Db 559 CGCGCGCGCGCGCTGAGCGTGGCCACCTTTCGCGCGGGCTACTCTGCGCGGTGCG 618
QY 654 CGCCACCTCGCGCTGTATGCGGCATGCTGCGGCACCTGCGGCGGCTGCGCGTGGCC 713
Db 619 CTTGGTAGCTGGCTTACGAGCGACGCTATGTTTCCT---ATGGCGCGCGGTGGTCC 675
QY 714 CGCGCGCGCGATAGCGCCCTGACGGGCGAGGTGTGGCAGAGCGCGAGGCGCGTGCG 773
Db 676 CGC-----GGGCGCGGCGAGCAGAGGCGCGCAGCGCGCGCGGCG 724
QY 774 GCGCAAGGTCTCGCGCTGGTGGCGCGCTGTGCTGTCTTTCGCGCGCTGTGCGGCGCC 833
Db 725 GG-----ACGSGCCATGTGCGAGTGGCGCGCTCTACGCGCTTTCGCGCGCGCC 774
QY 834 CATCAGCTGTTCTGGTCTGACGGCGTGGGCGCGCGCGGCTCTGSCACCCAGCGAG 893
Db 775 GCACCAACGCGCTCAT-----CCTCTGCTTCTGGTACGGTACGGTCTGCGCTTCAG 822
QY 894 CTACGCGCGCTTACGCGCTTAAGACCTTGGCTCACTGCAATGCTTACAGCAACTCGCGCT 953
Db 823 CCGGCGCACCTAGCGCTGTGCGCTGGCTCGCACTGCGCTGCTGCTAGCGCAACTCTGCT 882
QY 954 GAACCGCTGTCTACGCTTCTTGGGCTGCACTTCCGACAGGCTTCCGCGCGGTGTG 1013
Db 883 TAAACCGCTGTCTACTCTGCTGCGCTGCGCGCACTTCCGCGCGCTTCCGCGCGCTGTG 942
QY 1014 CCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1049
Db 943 GCGCTGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 978
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RESULT 7

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US-10-995-561-321
; Sequence 321, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
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RESULT 8

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US-10-995-561-320
; Sequence 320, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-321

Query Match 11.6%; Score 139.4; DB 7; Length 1238;
Best Local Similarity 52.1%; Pred. No. 3.6e-13;
Matches 377; Conservative 5; Mismatches 326; Indels 15; Gaps 3;

QY 2 TGCACACCGTGTCTACGTCCGACCCAAAGCGCTCTCTGGGGGCGACCCGGGCAACCGCTCCG 61
Db 91 TGCCCCCGGGGCGAGGAAGGGCTGGGAGCGGCTTGCCCTCTGCGCCATATGCCAGTA 150
QY 62 GCTGCCCGGGGTGTGGCGCAAGCGCTCGGACGGCCAGTCCCTTCGCCCGCGGGCGGTGG 121
Db 151 GCGCTCCCGGAGCGGAGGAGGCGGTGGCGGGGCC---CGGGGACGCGCGGGCGGCGG 207
QY 122 AGCGCTGGCTCGTGGCGCTCTTCTTCGGGGCGCTGATGCTGTGGCGCTGTGGGGAACCT 181
Db 208 GCATGGTGGCTATCCAGTGCATCTACGGCGCTGGTGTGCTGTGGGCTGTGTGGCAAG 267
QY 182 CGTGGTCACTCTACGTCTATCTGCCGCCAAGCCGATGCGGACCGTACGACCACTTCTACA 241
Db 268 CCTGGTCACTCTCTGTATCTCTCGTACGCGCAAGATGAAGACGGCTACCAACATCTACC 327
QY 242 TCGCAACCTGGCGGCCAGGAGCGTACCTTCTCTGTGTGCTGCTGCTTTCAGGCGCC 301
Db 328 TGCTCAACCTGGCGCTAGCGGACGAGCTCTTCACTGTG---AGCGTGGCTTCTGTCGCT 384
QY 302 TGCTGTACCCGCTGCCGCTGGGTGCTGGGGGAGTTCATGTGCAAGTTCGTTCACTACA 361
Db 385 CGTGGCGCGCTTGGCGCACGTGGCCCTTGGGCTCGGCTGTGTGGCGCGGCGGTGCTCAGCG 444
QY 362 TCACGACGCTCTCGGTGCGAGCGCACGTGTGCCACTCTGACCCGCCATGAGTGTGGACCGCT 421
Db 445 TCGACGGCTCAACATGTTTCAACGCGCTTCTGTCTCACCCTGCTCAGCGTGGACCGCT 504
QY 422 GGTAGTGAAGGTGTTCCTGTTGCGCGCTGTGCAACCGCGCACAGCCCGCTTGGCGCTGG 481
Db 505 AGTGGCGGTGTGACCGCTCTGCGCGGGCGCACCTACCGGGGCGCGCGCGTGGCCCAAGC 564
QY 482 CTGTGAGGCTCAGCATCTGGGTAGGCTCTGCGCGGCTGTCTGCGCGGCTGTGCGCGCTGC 541
Db 565 TCATCAACCTGGGCGTGTGGTGGCATCCCTGTGGTCACTCTCCCCATCGCCCATCTTCG 624
QY 542 ACCGCTGTCAACCCCGGCGCGCGCTA-----CTGCAGTGAAGGCTTCCCCCAGCG 592
Db 625 CAGACACACAGACCGGCTCGCGGGCGCAGGCGCTGCGCTGCAACCTGCACTGGCCACACC 684
QY 593 GCGCGCTGGAGCGCGCTTGGACATGTGTACAACTGCTGCGCGCTGTATCTGTGTCGCGCTGC 652
Db 685 GCGCGTGGTGGCAGTGTTCGTGTGTACTACTTCTCTGCTGGGCTTCTGCTGCGCGCTGC 744
QY 653 TCGCCACCTCGCGCTGCTATGCGGCGCATGCTGCGGCACCTGCGGCGGGTTCGCGCTGCGCG 712
Db 745 TGGCCATTTGGTGTGTGCTACTGCTCATCTGTGGGCAAGATGCGCGCGGTGGCGCTTGGCG 804
QY 713 CCG 715
Db 805 MKG 807
```



```

: TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
:
: TITLE OF INVENTION: DETECTION AND USES THEREOF
:
: FILE REFERENCE: C0601559
:
: CURRENT APPLICATION NUMBER: US/10/995,561
:
: CURRENT FILING DATE: 2004-11-24
:
: NUMBER OF SEQ ID NOS: 85702
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 320
:
: LENGTH: 1498
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-10-995-561-320

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Query Match	11.6%	Score 139.4	DB 7	Length 1498
Best Local Similarity	52.1%	Pred. No. 3.6e-13		
Matches	377	Conservative	5	Mismatches 326; Indels 15; Gaps 3
Qy	2	TGCACACGTCGTCACGTCGCCGACCCCAACGCGTCCTGGGGGGACACGGCCAAACGCTCCG	61	
Db	91			
Qy	62	GCTGCCCGGGTGTGGGCCCAACGCCCTCGAGACGGCCCAAGTCCCTTCGCGCGGGCCCGTGG	121	
Db	151			
Qy	122	ACGCCCTGGCTGTCGCGCTCTTCTTCGGGGCGCTGATGCTCTGGGCGCTGTGGGGAACCT	181	
Db	208	GCATGGTGGCTATCCAGTGCATCTACGCGCTCTGCTGGTGGGGCTGTGTGGGCAACG	267	
Qy	182	CGCTGGTTCATCTAGTGTATCTGCCGCCCAACGCGATGCGGACCGTGACCAACTTCTACA	241	
Db	268	CCCTGGTTCATCTTGTGATCCTTCGCTACGCCAAGATGAACCGGCTTACCAATCTTACC	327	
Qy	242	TGCGCAACCTGGCGGCCACGAGACGTGACCTTCTCTCTGTGTGGTCCCTTCACGGGCC	301	
Db	328	TGCTCAACCTGGCGGTAGCCACGAGCTCTTCATGCTG---AGCGTGCCTTCGTGGCGCT	384	
Qy	302	TGCTGTACTCCGCTCCCGGCTGGGTGCTGGGGGACTTCATGTGCAAGTTCGTCAACTACA	361	
Db	385	CGTCGGCGGCCCTGGCCACTTGGCCCTTCGGCTCCGTGCTGTGCCGCGGTGCTCAGCG	444	
Qy	362	TCCAGCAGGTCTCGGTGCAGGCCACGTGTGCGCACTCTGACCGCCATCAGTGTGGACCGCT	421	
Db	445	TCGACGGCCTCAACATGTTCAACAGCGTCTTCTGTCTCACCGTCTCAGCGTGGACCGCT	504	
Qy	422	GGTACGTGACGGTGTCCGTTTGGCGCCCTGCAACGGCGCACGCGCGCGCTGTGGCGGTGG	481	
Db	505	ACGTGGCGGTGGTGCAACCTCTGGCGCGCGACCTACCGCGCGCCACGCGTGGCCCAAGC	564	
Qy	482	CTGTGAGCCTCAGCATCTGGGTAGGCTCTCGCGCGGTGTCTGCGCGGTGTCTCGCCCTGC	541	
Db	565	TCATCAACCTGGGGTGTGGCTGGCATCCCTGTGGTCACCTCTCCCAATCCCATCTTTCG	624	
Qy	542	ACCGCTGTCAACCGGGCGCGCGCTA-----CTGCAGTGAAGCGCTTCCCCAGCC	592	
Db	625	CAGACACGAGACCGCTCGCGCGGCCAGAGCGGTGGCGTGCACCTGCAGTGGCCACACC	684	
Qy	593	CGCGCCTGGAGCGGCCTTCGCATGTATCAACCTGCTGGCGCTGTACCTGTCTGGCGGTGC	652	
Db	685	CGGCGCTGGTCGGCAGTCTTCTGGTGTACACTTTTCTGCTGGGCTTCTGTGTGGCGGTGC	744	
Qy	653	TCGCGCACTGCGCCTGTCTATCGCGCCATGCTGCGCCCACTGGGCGCGGTTCGCCGTGGGCC	712	
Db	745	TGGCCATTGGYCTGTGCTACCTGCTCATCTGTGGGCAAGATGCGCGCGTGGCCCTGTGGC	804	
Qy	713	CCG 715		
Db	805	MKG 807		

```

; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13298
; LENGTH: 86131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13298

Query Match      11.6%; Score 139.4; DB 7; Length 86131;
Best Local Similarity 52.1%; Pred. No. 2.8e-13;
Matches 377; Conservative 5; Mismatches 326; Indels 15; Gaps 3;

Qy      2   TGCACACCGTGGCTACGCTCGGACCCAAACGCGTCTCGGGGGGACACGGGCAACGCGCTCCG 61
Db      6092 TGCCCCCGGGGCGAGGAAGGCTGGGAAGCGCCTTGCGCCCTCTGCAGCAATGCCAGTA 6151

Qy      62   GCTGCCCGGGCTGTGGCGCCAAACGCTTCGGA CGGCCAGTCCCTTCGCCGCGGGCCGCTGG 121
Db      6152 GCGCTCCGGCGAGGCGGAGGCGGTGGCGGGGC---CGGGAGACGGCGGGCGGCGCG 6208

Qy      122  ACGCCTGGCTCGTGGCGCTCTTCTTCGCGCGCTGATGCTGTGGCGCTGGTGGGGAAC 181
Db      6209 GCATGGTCGCTATCCAGTGCATCTACGCGTGGTGTGCTGTGGGGCTGTGGGCAACG 6268

Qy      182  CGCTGGTGCATCTACGTCACTGCGGCCACAAGCCGATGCGGACCGTGACCACTTCTACA 241
Db      6269 CCCTGGTGCATCTTCGTGATCTTTCGCTAGCCCAAGATGAAGACGGCTACCAACATCTACC 6328

Qy      242  TCGCCAACTGGCGGCCACA CGGACGTGAACCTTCTCTGTGCTGCTGCTGCCCTTTCACGGCCC 301
Db      6329 TGCTCAACTGGCGCGTAGCGACGAGCTCTTCAATGCTG---AGCGTGCCCTTCGTGGCCT 6385

Qy      302  TGCTGTACCCGCTGCCCGGCTGGGTGCTGGCGACTTCATGTGCAAGTTTCGTCAATACA 361
Db      6386 CGTGGCGCGCCTTGGCGCACTGGCCCTTGGCTTCGCTGTGTCGGCGGGTGTCTCAGCG 6445

Qy      362  TCCAGCAGGTCTCCGTTGCAGGCCACAGTGTGCCACTCTGACCGCCATAGTGTGGACCGCT 421
Db      6446 TCGACGCGCTCAACATGTTTAC CAGCGTCTTCTGTCTCACCGTGTCTCAGCGTGGACCGCT 6505

Qy      422  GGTAGTGACGTTTCCGTTGGCGGCCCTGCACCGCGCAGCCCCCGCTGGCGCTGG 481
Db      6506 ACGTGGCCGTGTGCACCCCTTCGCGCGCGCGCACTTACCGCGCGGCCACGCTGGCCCAAGC 6565

Qy      482  CTGTGAGCTCAGCATCTGGGTAGGTCTTCGCGCGGTGTCTGCGCGGTGTCTCGCCCTGC 541
Db      6566 TCATCAACCTTGGCGGTGTGGCTGCATTCCTGTGTGTACTCTCCCATCGCCATCTTTCG 6625

Qy      542  ACCGCTGTACCCGGGCGCGCGCTA-----CTCAGTGAAGGCTTCCCCAGCC 592
Db      6626 CAGACACCAACACCGGCTTCGGCGCGCGCAGCGCTGGCCCTGCAACTGCAGTGGCCACACC 6685

Qy      593  GCGCCCTGGAGCGGCTTTCGCACTGTACAACTGTGTGGCGCTGTACTCTGCTGCCCTGC 652
Db      6686 CGGCCCTGGTCGAGTATTCGTGGTCTACACTTCTGTGTGGCTTCTGCTGCCCTGC 6745

Qy      653  TCGCCACTCGCCTGTATGCGGCCATGTGTCGCCACCTGGGCGGGCTCGCCGTGGCC 712
Db      6746 TGGCCATTGTCGTGTACTCTCTCATCGTGGGCAAGATGCGCGCGCTGCCCTGTGCG 6805

Qy      713  CCG 715
Db      :
Db      6806 MKG 6808

```

Query Match	11.2%;	Score 134.6;	DB 11;	Length 2327;
Best Local Similarity	55.3%;	Pred. No. 1.8e-12;		
Matches 328;	Conservative 1;	Mismatches 250;	Indels 14;	Gaps 3
Qy	115	GCCTGTGGACGCGCTGGCTCGTGC	CGCTCTTCTTCGCGGCGCTGATGCTGCTGGCGCTGGT	174
Db	327	GGCGTGGAGAACTTCATCACGCTGGTGGTGT	TTTTCGCGATGGCGGTGCTG	386
Qy	175	GGGAACCTGCGTGGTTCATCTAGCTCATCTG	CGCCCAAGCC-----GATCGGAGCCGTCG	228
Db	387	GGCAACAGCCTGGTGATCACCGTGTGCGCGC	GACAAACCGGCAAGCCGCGCAGCACC	446
Qy	229	ACCAACTTCATACATGCCAACCTGGCGGCGCA	CGGACGTGACCTTCTCTGTGCTGCGTC	288
Db	447	ACCAACCTGTTTCATCTCTCAACTCGAGCATCG	CAGACCTGGSGCTACTCTCTCTTCGTGCATC	506
Qy	289	CCCTTCACGGCCCTGCTGTACCGCTGCGCGCT	GGGTGGTGGGCGACCTTCATGTGCAAG	348
Db	507	CCCTTCACGGCCACCGTGTACGCACTGCCCACT	GGGTGGTGGGCGCTTCATCTGCAAG	566
Qy	349	TTCTGTCAACTACATCCAGCAGGTCTCGGTG	CAGGCCACCGTGTGCCACTCTGACCGCCATG	408
Db	567	TTTATACACTACTTCTTACCGTGTCCATGTCTG	TGAGCATCTTCACCTGGCCGCGATG	626
Qy	409	AGTGTGACCGCTGGTACGTGACGGTGTTC	CGGTTCGCGCCCTGTGCAACCGCGCACGCC	468
Db	627	TCTGTGATCGCTATGTGGCCATTTGTGCA	TTCACGGCTCTCTCCCTCAGGGTGTC	686
Qy	469	GGCCTGGCGCTGGCT--GTACGCTCAGCATCT	GGGTAGGCTCTGCGGCGGTGTCTGGC	526
Db	687	CGCCAAACGCGCTGTGGGCGTGGGCGCTTCATCT	GGGCGCTGTCCATGCTATGGCCTCGC	746
Qy	527	CGGTGTGCGCCCTGCACCGCTGTCCACCGCG	CGCGCGC-----GCCTACTGCAGTAGG	580
Db	747	CGGTGGCTACTACGAGGCGCTTTTTCATCGGGA	CAGCAACCAACCTCTCTGCTGGGAGC	806
Qy	581	CTTTCCCAGCGCGCCCTGGAGCGCGCTTC	TGCACTGTACAACTCTGTCGGCGCTGTACC	640
Db	807	ACTGGCCCAACCAACTCCACGAAGGCTTACGT	GGTGTGTCATCTTCTGTTTACC	866
Qy	641	TGCTGCGGCTGCTGCCACCTGCGGCTGCTATG	CGGCGCATGCTGGCGCACCTG	693
Db	867	TTCTGCCCTTACTGCTCATCTGCTTTTTCGTATG	CCCAAGTTCTCAATCATCTG	919

RESULT 11
US-10-750-185-36071/c
; Sequence 36071, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

; APPLICANT:	DENISE, Sue K.
; APPLICANT:	KERR, Richard
; APPLICANT:	ROSENFELD, David
; APPLICANT:	HOLM, Tom
; APPLICANT:	BATES, Stephen
; APPLICANT:	FANTIN, Dennis
; TITLE OF INVENTION:	COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE:	MM1100-2
; CURRENT APPLICATION NUMBER:	US/10/750,185
; CURRENT FILING DATE:	2003-12-31
; PRIOR APPLICATION NUMBER:	US 60/437,482
; PRIOR FILING DATE:	2002-12-31
; NUMBER OF SEQ ID NOS:	64922
; SOFTWARE:	PatentIn version 3.1
; SEQ ID NO	36071
; LENGTH:	1685
; TYPE:	DNA
; ORGANISM:	Bovine
US-10-750-185-36071	19866880675545

Query Match	9.2%;	Score 110.2;	DB 7;	Length 11
Best Local Similarity	51.6%;	Pred. No. 8.7e-09;		
Matches 312;	Conservative 0;	Mismatches 278;	Indels	

QY	123	CGCCTGGGTCGTGGCGGCTCTTCTTGCGCGCGCTGATGCTCTGGGCGCTCG
Db	1342	CGTATCTCATCTCTTTTCATCTACTTCCGTGGTGTGCTCGTGGGCGCTC
QY	183	GCTGTGCATCTACGTCACTGCGGCCACAAGCCGATGCGGACCGTGACCGTGCACC
Db	1282	CATGTCATCTACGTGATCTCTGGCTACGCCAAGATGAACAGCGSCCAC
QY	243	CGCCAACTGGCGGCCACGGAGCTGACCTTCTCTCTGTGCTGTGCTGCTGCC
Db	1222	CCTCAACCTGGCCATTCGCGGATGAG---CTGCTCATGCTCAGCGTGCCCT
QY	303	GCTGTACC CGCTGCCC GGCTGGGTGCTGGCGGACTTCATGTGCAAAGTTTC
Db	1165	CTCCATATGCTTCGCCACTGCCCCCTTCGCGGGCTACTCTGCGGCTCTC
QY	363	CCAGCAGTCTCGGTGTCAGGCCACGCTGTGCCACTCTGACCGCCCATGATGT
Db	1105	GGAGCAGTCAACATGTTTCAACCAGCATCTACTGTCTGACTGTGTGCTTAGCC
QY	423	GTA CGTGACG GTTTC CCGTTC GCGCCCTGCACCGCCGCGCATCGCCCGCCG
Db	1045	CGTGCCGCTGTGTGCACCCCATCAAGCGCCGCA CGCTACCGCGCGGCCACCC
QY	483	TGT CAGCCTC A GCA TCTGGT AGGCTCTGCGGCGGTGTCTGCGCCGGTGAGC
Db	985	GGTGNATCTGGGCTGTGGGTGCTGTGCTGCTCTGTCATTCTGCCCCATTC
QY	543	CCGCTGTGACC-----CGGCGCGCGCGCTACTGTGAGTGAGAGG
Db	925	GCGCAGCGGCGCAACAGCAGCGGACGGTGGCTTGCAACATGCTCATGTG
QY	591	CCGGCCCTTGAGCGCGGCTTCGCAC TGTA CAACCTGTGCTGGCGCTGTGAC
Db	865	CCAGCGCTGGCTGTGGGCTTCGTGTGTGACACTTTTCTCATGGGCTTC
QY	651	GCTCGCCACTCGCGCTGCTATGTCGGGCCATGTGCGGCCACTTGGGCGGGGCG
Db	805	CGGGGCCATCTGCTTGTGTCTAGCTGCTCATCATCGCCAAAATGGCGATG
QY	711	CCCCG 715
Db	745	GGCCG 741

RESULT 12
US-10-750-623-36071/c
; Sequence 36071, Application US/10750623
; Publication No. US20050287531A1

```
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-623-36071

Query Match      9.2%; Score 110.2; DB 7; Length 1685;
Best Local Similarity 51.6%; Pred. No. 8.7e-09;
Matches 312; Conservative 0; Mismatches 278; Indels 15; Gaps 2;

Qy 123 CGCTGTGCTGTCGCGCTCTTCTTCGCGCGCTGATGCTGTGGCCCTGGTGGGAACTC 182
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1342 CGCTATCTCATCTCTTTTCATCTACTCCGTGGTGGCTGGTGGGGCTCTGTGGAACTC 1283
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 193 GCTGGTATCTACGTCACTCGCGCCACAGCCGATGGGACCGTGACCACTCTTACAT 242
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1282 CATGGTCACTACGTGATCTCGCGCTACGCCAAGATGAAGACGGCCACCAATCTACAT 1223
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 243 CGCCAACTGGCGGCGACGAGCTTCTCTCTGTGCTGCGTCCCTTTACGGCCCT 302
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1222 CCTCAACTGGCATCGCCGATGAG--CTGCTATGCTAGCGTGCCCTTCTGGTCA 1166
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 303 GCTGTACCCGTGCGCGCTGGTGTGGGCGACTTCAATGCAAGTTGTCAATACAT 362
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1165 CTCACATGCTTCGCCACTGGCCCTTCGGCGCGTACTCTGCGCGCTCGTCAAGGT 1106
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 363 CCAGCAGTCTCGGTGAGGCGACGTGTGCCACTCTGACCCGCATGATGTGGACCGTG 422
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1105 GGACGCACTCAACATGTTTCAACAGCATCTACTGTCTGACTGTGTTAGCGTGGACCGCTA 1046
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 423 GTACGTGACGGTGTTCGGGTTTGGCGCTTGACCGCGCACGCGCCCGCTGGCGCTGGC 482
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1045 CGTGGCGGTGTGACCCCATCAAGGCCGCGAGCTACCGCGCGCCACCGTGGCCAGGT 986
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 483 TGTACGCTCAGCATCTCGGTAGGCTTGGCGCGGTGTCTGCGCGGTGTCTGCGCCCTGCA 542
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 985 GGTGAATCTGGCGGTGGTGGTGTCTGCTGCTGCTCATCTGCGCATGTGTCTTCTC 926
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 543 CGGCTGTACC-----CGGCGCGCGCCCTACTGCGAGTGAGGCGCTTCCCGAG 590
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 925 GCGCAGCGCGCCAAACAGCGACGGCACGGTGGCTGCAACATGTCTATGCGCGAGCCCGC 866
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 591 CCGCGCCCTGAGCGCGCTTCGCACTGTACAACTGTCTGGCGGTGTACTCTGTGCGCGCT 650
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 865 CCAGCGCTGGCTGGTGGCTTCGTGTGTGTACATTTCTCATGGGCTTCTGCTGCGCGT 806
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 651 GCTGCCACCTGCGGCTGCTATGCGGCCATGCTGCGGCCACCTGCGGCGGGTTCGCGTGC 710
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 805 CCGGCGCATCTGCTGTGCTACTAGTCTCATCATCGCCAAATGCGCATGTGTGGCCCTCAA 746
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 711 CCCC 715
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 745 GGCCG 741
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-508-892-1

; Sequence 1, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; FILE REFERENCE: Neuropeptide FF Receptor 1 (NPFF1)
; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-508-892-1

Query Match      9.1%; Score 108.4; DB 6; Length 1293;
Best Local Similarity 47.4%; Pred. No. 1.6e-08;
Matches 473; Conservative 0; Mismatches 501; Indels 24; Gaps 4;

Qy 144 CTTGCGCGCGTGAATGCTGTGGCGCTGTGGGAACTCGCTGTGTCATCTACGTCACTCG 203
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 147 CTATGCGCTCATCTTCCTGCTCTGTCATGGTGGGCAACACCCCTGTCTGTTTCATCGTCT 206
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 204 CGGCCAACAGCCGATGGGACCGTGACAACTTCTATATGCCCAACCTTGGGGCCACGGA 263
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 207 CAAGAACCGGCACATGATCTGTCAACATCTTCACTCAACCTTGGCTGTCAGTGA 266
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 264 CGTGACCTTCTCTGCTGTGCGTCCCTTACCGCCCTGTGTACCGCTGCCCGCTG 323
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 267 CTTGCTGGTGGCATCTTCTGTCATGCCACACCCCTTGTGGACAACTCATCTACCTGGTG 326
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 324 GGTGCTGGGGCATCTTATGTGCAAGTTTCGTAACATCCAGCAGGTCTCCGTGTCAGGC 383
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 327 GCCCTTCGACAAATGCCACATGCAAGATGAGCGGCTTGGTGCAGGGCATGTCTGTGCGGC 386
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 384 CAGCTGTGCCACTCTGACCGCATGATGTGTGACCCGTGTGTAAGTGTGAGTGTTCCTGTT 443
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 387 TTCGCTTTTCACTGCTGTGGCCATTTGTGTGGAAGGTTCCGCTGTCATCTGTGCACTCTT 446
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 444 GCGCG---CCCTGCACCGCGCAGCCCGCTGCGCTGGCTGTGCTCAGCTCAGCATCTG 500
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 447 CCGCGAAGCTGACCTGCGGAAGGCGCTCGTCAACATCGCCGTCATCTGGGCGCTGGC 506
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 501 GGTAGGCTCTGCGCGCGTGTCTGCGCGCGTGTCTGCGCTGTCAGCCGCTGTCAACCGGCGC 560
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 507 GCTGCTCATATGTGTCTTCCCTCGGCCGTCACTGACCGTCAACCGTGTGAGGAGCACCATT 566
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 561 GCGCGCTCATGTAGTGTGAGGCTTCCCGAGCCGCGCTGTGAGCGCGCTTGGCACTGTA 620
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 567 CATGGTGTGAGCGCGCAACCGCTCTACCTCTCTACTCTGTGTGGAGGCTGTGGCCGA 626
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 621 CAACCTGTGCGGCTGTACCTGTGCGCTGTCTGCGCAACCTGTGCGCTGTATGCGGCCAT 680
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 627 GAAGGGCATGCGAGGGTGTACACCATGTGTCTTTCTGACATATACCTGTGGCGCGCT 686
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 681 GCTGCGCCACCTGGCGCGGGTTCGCC-----GTGCGCGCGCGCGCGCGCGCG 725
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 687 GCGGCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 726 TAGCGCCCTGTGAGGGGAGGTGTGTGGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 785
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 747 GGCCCGCGCGCGCGAGGAGGTGTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 806
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 786 GCGGCTGTGGCGCGCGGTGTCTGCTCTTTCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCG 845
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 807 GCACATGCTGGTGCATGGTGGCGCTGTCTTTCACGCTGTCTCGGCTGCCGCTCTGGGGCGCT 866
Qy 846 CTTGCTGCTGCAGCGCTGGGCGCCCGCGGCTCTTGGCACCCACGAGCTAGCGCGCTTA 905
Db 867 GCTGCTGCTCATGACTACGGGAGCTCAGGGCGCGGAGCTGCACCTGGTCAACGCTCTA 926
Qy 906 CGGCTTAAGACTGGGCTACCTGATGCTCTACAGCAACTCGGCGCTGAACCCGCTGCT 965
Db 927 CGCCTT---CCCCTTCGCGCACTGGCTGGCTTCTTCAACAGCAGCGCCAAACCCCATCAT 983
Qy 966 CTACGCTTCTCTGGGCTCGCACTTCGACAGGCGCTTCGCGCGCTGTGCGCGCC 1025
Db 984 CTACGCTACTTCAACAGAGACTTTCGCGCGGCTTCCAGGCGCGCTTCC---GGCGCG 1040
Qy 1026 GCG 1085
Db 1041 CCTTGGCG 1100
Qy 1086 GCTGACCGCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1123
Db 1101 TCTGCACAGCGCGGCTCTCTGTGTGTGGCGCGCGCGCGCGCGCGCGCGCG 1138

RESULT 14

US-10-992-577-7 ;
; Sequence 7, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JFW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1998-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-992-577-7

Query Match 9.1%; Score 108.4; DB 7; Length 1293;
Best Local Similarity 47.4%; Pred. No. 1.6e-08;
Matches 473; Conservative 0; Mismatches 501; Indels 24; Gaps 4;
Qy 144 CTTGCGGCGCTGATGCTGCTGGCGCTGGTGGGAACTGGCTGCTGCTATCTAGTCACTG 203
Db 147 CTATGGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
Qy 204 CGGCACAGCGGATGCGGACCGTGCACAACTTCTACATCGCAACCTGGCGGCGCACGGA 263
Db 207 CAAGAACCGGACATGATCTGTACCAACATGTTCACTCAACCTGGCTGTCAAGTGA 266
Qy 264 CTTGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
Db 267 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326
Qy 324 GGTGCTGGCGACTTCATGTGCAAGTTGTTCACTACATCAGCAGGCTCTGGTGCAGGC 383
Db 327 GCCCTTCGACAAATGCCACATGCAAGATGAGCGGCTTGGTGCAGGCGATGTCTGTGCGC 386

Qy 384 CACGTGTGCCACTCTGACCGCCATGAGTGTGGAACCGCTGGTACGTGACGGTGTTCCTCGGTT 443
Db 387 TTCCGTTTTCACACTGGTGGCCATTTGCTGTGGAAGGTTCCTGCTCATCTGTCACCCCTTT 446
Qy 444 GGGCG---CCCTGACACCGCGGACCCCGCGCTGGCGGTGGTGTGACGCTCAGCATCTG 500
Db 447 CGCGAGAGAGCTGACCTCTGCGAGAGCGCTCTGTCACCATCGCCGCTCATCTGGCGCGCTG 506
Qy 501 GGTAGGCTCTGCGGGGCTGCTGCGCGGTGCTGCGCGCTGCTGCGCGCTGCTGCGCGCG 560
Db 507 GCTGCTCATGATGTGCTGCTGCGCGGTGCTGCGCGGTGCTGCGCGGTGCTGCGCGGT 566
Qy 561 GCGCGCTTACTGCACTGAGGCGCTTCCCGAGCGCGCGCTTGGAGCGCGCTTCCGCACTGTA 620
Db 567 CATGCTGAGCGCGCGCAACCGCTCTACTCTCTACTCTCTGCTGGAGGCTTGGCGCGA 626
Qy 621 CAACCTGCTGGCGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
Db 627 GAAAGGCTGCGGAGGCTTACACCATGCTGCTCTCTGCGACATCTACTGCGCGCTG 686
Qy 681 GCTGCGCGCGCTGCGCGGCTGCGCG---GTGCGCGCGCGCGCGCGCGCGCGCGCG 725
Db 687 GCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
Qy 726 TAGCGCTCTGAGGCGGAGGCTGCTGCGAGAGCGCGCGCGCTGCGCGCGCGCGCGCGCTC 785
Db 747 GCGCGCGCGCGCGGAGGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 806
Qy 786 GCGGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
Db 807 GCACATGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
Qy 846 CTTGCTGCTGAGGCGCTGGGCGCGCGCGCGCGCTGCTGCGACCGCGCGCTGCTGCGCGCT 905
Db 867 GCTGCTGCTCATGCACTACGCGCGAGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCT 926
Qy 906 CGCGCTTAAGACCTGGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965
Db 927 CGCCTT---CCCTTCTGCGCACTGGTGGCTTCTTCAACAGCAGCGCGCGCGCGCGCTCAT 983
Qy 966 CTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1025
Db 984 CTACGCTTACTTCAACGAGAACTTCCGCGCGCGCTTCCAGGCGCGCTTCC---GCGCGCG 1040
Qy 1026 GCG 1085
Db 1041 CCTTGGCGCGCGCGCGCTGCGGAGCGCAACAGGAGGCGCTTCTCCGAGCGCGCGCGCGCT 1100
Qy 1086 GCTGACCGCTGGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1123
Db 1101 TCTGCACAGCGCGGCTCTTCTGTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1138

RESULT 15

US-11-136-527-463
; Sequence 463, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 463
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-11-136-527-463

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Query Match          9.0%; Score 107.4; DB 11; Length 1350;
Best Local Similarity 51.6%; Pred. NO. 2.3e-08;
Matches 246; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

Qy 132 CGTGGCGCTCTTCTCGCGCGCTGATGCTGCTGGGCTGTGGGACTCGCTGGTCAT 191
Db 132 CGTACCGCCACCTGCGGCGCTCTTCTGGTGGGCATCTCAGGCAACCTGCTCACTAT 191

Qy 192 CTAGCTCATCTGCGGCCACAAGCCGATCGGACCGTGAACCACTTCTACATCGCAACCT 251
Db 192 GCTGTGTGTCTCCCGCTTCGCGGAGCTGGGACACCAACCACTTCTACCTGTCCAGCAT 251

Qy 252 GGGGCCACGAGAGTGACCTTCTCTCTGTGTGGTCCCTTTCAGGGCCCTGCTGTACCC 311
Db 252 GGCCTTCTCGGATCTGCTCATCTTCTCTGTGATGCCGCTGGACCTCGTCCGCTCTGGCA 311

Qy 312 GCTGCCCGCTGGGTGCTGGGGACTTCTATGTGCAAGTTCTCAACTACATCCAGCAGGT 371
Db 312 GTACCGGCCCTGGAACTTCGGGGAACCTGCTCTGCAAACTCTTCCAGTTTGTACGCGAGAG 371

Qy 372 CTCGGTGCAGGCCACGCTGTGCCACTCTGACCGCCATGAGTGTGACCGCTGCTACGTGAC 431
Db 372 CTGCACCTACGCCACGGTCTCTACCATCACCGCGCTGAGCGTGGAGCGCTACTTGGCCAT 431

Qy 432 GGTGTTCCGTTGGCGCCCTTGACCCGCCGACCGCCCGCTGGCGCTGGCTGTGAGCCT 491
Db 432 CTGCTTCCCTCTGCGGGCCAAAGTGGTGGTCACTAAGGGCCGCGTGAAGCTGGTCACTCCT 491

Qy 492 CAGCATCTGGGTAGGCTCTGCGGGGGTGTCTGCGCCGGTGTCTGCCCCCTGCACCCGCTGTC 551
Db 492 TGTCACTCTGGGCGCGTGGCTTTCTGCAGCGCGGGGCCCATCTTCTGCTGTGGTGGCGTGA 551

Qy 552 ACCCGGGCGCGCGCTTACTGCAGTGAGGCTTCCCCAGCGCGCCCTTGGAGCGCGC 608
Db 552 GCACGAAACCGCACAGATCCCGGGACACCAACGATGCCCGGCCACCGAGTTCCG 608
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Search completed: February 15, 2006, 03:34:10
Job time : 337 secs